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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:09:28 ; Search time 32.4 Seconds
(without alignments)
24.676 Million cell updates/sec

Title: US-09-600-432-24
Perfect score: 32
Sequence: 1 PRARIY 6

Scoring table: BLOSUM62
Gapop.10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 42205

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq.101002:*

1:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
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3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
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14:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
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18:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	6	20 AAY28511	Beta-1 integrin ce
2	32	100.0	6	21 AAB19065	Amino acid sequenc
3	25	78.1	5	18 AAW19842	Chimeric adenoviru
4	25	78.1	5	20 AAY28512	Beta-1 integrin ce
5	25	78.1	5	20 AAY28546	Beta-1 integrin ce
6	25	78.1	5	21 AAB19066	Amino acid sequenc
7	25	78.1	5	21 AAB19067	Amino acid sequenc
8	20	62.5	4	20 AAY28513	Beta-1 integrin ce
9	20	62.5	4	21 AAB19068	Amino acid sequenc
10	19	59.4	6	20 AAY25842	Human secreted pro

11	18	56.2	5	19	AAV21060	Human p53 cellular
12	18	56.2	5	19	AAW74620	Analogue of chymot
13	18	56.2	5	22	AAE11144	Chymotryptic pepti
14	18	56.2	5	23	AAE24433	Transporter peptid
15	17	53.1	5	6	AAP50198	Sequence of oligop
16	17	53.1	5	19	AAW74622	Analogue of chymot
17	17	53.1	5	22	AAW48782	Human saliva PRP-1
18	17	53.1	5	22	AAW55601	Human saliva PRP-1
19	17	53.1	5	22	AAW57448	T cell surface rec
20	17	53.1	5	22	AAW57858	DNAM-1 C-terminal
21	17	53.1	5	22	AAW08720	Trypsin inhibitory
22	17	53.1	6	17	AAW08721	Trypsin inhibitory
23	17	53.1	6	17	AAW08722	Trypsin inhibitory
24	17	53.1	6	17	AAW08722	S. acidocaldarius
25	17	53.1	6	18	AAW15886	Peptide derivative
26	17	53.1	6	19	AAW80768	Heparin sulfate bi
27	17	53.1	6	19	AAW56944	Enzyme inhibitor p
28	17	53.1	6	20	AAV50279	Neutrophil-activat
29	17	53.1	6	20	AAV50279	Fibronectin peptid
30	17	53.1	6	21	AAW01581	Proteoglycan bindi
31	17	53.1	6	22	AAW48781	Human saliva PRP-1
32	17	53.1	6	22	AAW55602	DNAM-1 C-terminal
33	17	53.1	6	22	AAW57449	T cell surface rec
34	17	53.1	6	22	AAW57859	DNAM-1 C-terminal
35	17	53.1	6	23	AAU85707	Extra cellular mat
36	17	53.1	6	23	AAU11029	Recombinant RSV ge
37	16	50.0	4	10	AAW1620	Motif useful in to
38	16	50.0	4	13	AAW21664	Cyclic tetrapeptid
39	16	50.0	4	19	AAW55761	Immunisation motif
40	16	50.0	4	20	AAW42612	Human IgE peptide
41	16	50.0	4	21	AAW85252	Human IgE mutant #
42	16	50.0	4	22	AAW86383	Cathepsin derived
43	16	50.0	4	23	AAU79083	Thrombin inhibitor
44	16	50.0	5	5	AAP40816	Sequence of fragme
45	16	50.0	5	7	AAP60156	Human growth hormo

ALIGNMENTS

RESULT 1
AAY28511
ID AAY28511 standard; peptide; 6 AA.
AC AAY28511;
XX
XX
DT 19-OCT-1999 (first entry)
XX
XX Beta-1 integrin cell adhesion modulator analogue #24.
DE Beta 1 integrin dependent cell adhesion; LipAR motif; tumour;
KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
XX
XX Synthetic.
XX
XX WO9937669-A1.
XX
XX 29-JUL-1999.
XX
XX 21-JAN-1999; 99WO-US01236.
XX
XX 12-AUG-1998; 98US-0096212.
XX
XX 22-JAN-1998; 98US-0072119.
XX
XX 12-AUG-1998; 98US-0096211.
XX
XX (MINU) UNIV MINNESOTA.
XX
XX Brienzo A, Furcht LT, McCarthy JB;
XX
XX WPI; 1999-469112/39.
XX
XX New peptides modulating beta1 integrin subunit dependent cell
PT adhesion, useful to study cell adhesion e.g. alpha4beta1 integrin

PT dependent adhesion important in tumour cell biology
 XX Claim 6; Fig 7; 47pp; English.
 XX This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AY28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which
 CC has a side chain including an aromatic group, and a penultimate
 CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
 CC a 'LipAr' motif. Studies with these peptides have also shown that
 CC inhibiting peptides do not contain D-amino acids and that it is the
 CC presence of the ArLip motif that conveys effective beta1 integrin
 CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
 CC cell adhesion is important for cell adhesion to extracellular matrix
 CC proteins, and the subunit is expressed on tumours such as melanomas.
 CC Therefore these LipAr motif containing peptides may be important in the
 CC treatment of cancer.
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 32; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRARIY 6
 Db 1 PRARIY 6
 DE Amino acid sequence of a beta1-integrin inhibitor.
 XX Beta1-integrin inhibitor; leukocyte mediated tissue destruction;
 KW central nervous system ischemic injury; myocardial infarction;
 KW beta1-integrin; angioplasty; surgical incision; injury-related trauma;
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX Synthetic.
 OS WO200056350-A2.
 PN 28-SEP-2000.
 XX 22-MAR-2000; 2000WO-US07680.
 PF 22-MAR-1999; 99US-0125634.
 PR 24-NOV-1999; 99US-0167538.
 XX (MINU) UNIV MINNESOTA.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (SENT-) SENTRON MEDICAL INC.
 XX McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
 PI Furcht LT;
 XX WPI; 2000-656062/63.
 DR Inhibition of inflammatory leukocyte mediated destruction of tissue in
 XX a patient, comprises administering a peptide inhibitor of
 PT beta1-integrin, useful for treatment of e.g. cancer and osteoporosis -
 PT Claim 3; Page 38; 61pp; English.
 XX AAB19054-67 represent beta1-integrin inhibitors. The peptides inhibit
 CC beta1-integrin which is responsible for leukocyte mediated tissue

CC destruction. The peptides are useful for inhibiting inflammatory
 CC leukocyte mediated destruction of tissue which occurs as a result of
 CC central nervous system (CNS) ischemic injury, myocardial infarction,
 CC angioplasty, surgical incisions, injury-related trauma, and/or
 CC transplant reperfusion, exposure to heat, cold, light, electricity
 CC and/or chemicals. They are also useful for the treatment of stroke, a
 CC burn type injury, cancer, and osteoporosis.
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 32; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRARIY 6
 Db 1 PRARIY 6
 DE Chimeric adenovirus coat protein heparin binding motif.
 XX Adenovirus; vector; coat protein; gene therapy; gene transfer;
 KW human; cancer; autoimmune disease; heart disease; infection;
 KW Heparin.
 XX Synthetic.
 OS WO9720051-A2.
 PN 05-JUN-1997.
 XX 27-NOV-1996; 96WO-US19150.
 PF 21-AUG-1996; 96US-0701124.
 PR 28-NOV-1995; 95US-0563368.
 XX 21-AUG-1996; 96US-0700846.
 XX (GENV-) GENVEC INC.
 XX Brough DE, Kovesdi I, Wickham TJ;
 PI WPI; 1997-310606/28.
 DR Adenoviral vectors containing chimeric coat protein - bind and enter
 XX cells more efficiently, useful for gene therapy of e.g. cancer,
 PT autoimmune diseases, etc.
 XX Claim 7; Page 19; 121pp; English.
 XX This peptide is used as a universal transfer vector (UTV) sequence
 CC or as a spacer sequence in novel chimeric adenovirus coat proteins
 CC (CP), especially chimeric fibre proteins. It comprises a heparin
 CC binding motif derived from fibronectin. Claimed UTVs/spacers are
 CC given in AAW19810-11, AAW19813-25, AAW19827, AAW19829, AAW19831-32 and
 CC AAW19834-43). Claimed chimeric CPs differ from the wild-type CP by the
 CC introduction of the UTV and/or spacer at or near the C-terminus or
 CC in an exposed loop. This imparts on the chimeric CP the ability to
 CC bind to and enter cells by means of a novel cell surface binding
 CC site. Recombinant vectors comprising the chimeric CP are able to
 CC enter cells more efficiently than vectors comprising wild-type CP,
 CC especially at lower m.o.i. They are especially useful for gene
 CC therapy of e.g. cancers, genetic disorders, pathogenic infections,
 CC heart disease or autoimmune diseases.
 XX SQ Sequence 5 AA;

Query Match 78.1%; Score 25; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRARI 5
 |||||
 Db 1 PRARI 5

RESULT 4
 AAY28512
 ID AAY28512 standard; peptide; 5 AA.
 XX
 AC AAY28512;
 XX
 DT 19-OCT-1999 (first entry)
 XX
 DE Beta-1 integrin cell adhesion modulator analogue #25.
 XX
 KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX
 OS Synthetic.
 XX
 PN WO9937669-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 21-JAN-1999; 99WO-US01236.
 XX
 PR 12-AUG-1998; 98US-0096212.
 PR 22-JAN-1998; 98US-0072119.
 PR 12-AUG-1998; 98US-0096211.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Brienzo A, Furcht LT, McCarthy JB;
 XX
 DR WPI; 1999-469112/39.
 XX
 PT New peptides modulating betal integrin subunit dependent cell
 PT adhesion, useful to study cell adhesion e.g. alpha4betal integrin
 PT dependent adhesion important in tumour cell biology
 XX
 PS Claim 6; Fig 7; 47pp; English.
 XX
 CC This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAY28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which
 CC has a side chain including an aromatic group, and a penultimate
 CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
 CC a 'LipAr' motif. Studies with these peptides have also shown that
 CC inhibiting peptides do not contain D-amino acids and that it is the
 CC presence of the ArLip motif that conveys effective betal integrin
 CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
 CC cell adhesion is important for cell adhesion to extracellular matrix
 CC proteins, and the subunit is expressed on tumours such as melanomas.
 CC Therefore these LipAr motif containing peptides may be important in the
 CC treatment of cancer.
 XX
 SQ Sequence 5 AA;

Query Match 78.1%; Score 25; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARIY 6
 |||||
 Db 1 RARIY 5

RESULT 5
 AAY28546
 ID AAY28546 standard; peptide; 5 AA.
 XX
 AC AAY28546;
 XX
 DT 19-OCT-1999 (first entry)
 XX
 DE Beta-1 integrin cell adhesion modulator analogue #39.
 XX
 KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX
 OS Synthetic.
 XX
 PN WO9937669-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 21-JAN-1999; 99WO-US01236.
 XX
 PR 12-AUG-1998; 98US-0096212.
 PR 22-JAN-1998; 98US-0072119.
 PR 12-AUG-1998; 98US-0096211.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Brienzo A, Furcht LT, McCarthy JB;
 XX
 DR WPI; 1999-469112/39.
 XX
 PT New peptides modulating betal integrin subunit dependent cell
 PT adhesion, useful to study cell adhesion e.g. alpha4betal integrin
 PT dependent adhesion important in tumour cell biology
 XX
 PS Example 11; Fig 15; 47pp; English.
 XX
 CC This peptide is used with AAY28510-Y28549 to show that peptides
 CC which modulate beta-1 integrin subunit dependent cell adhesion need a
 CC C-terminal amino acid residue (Ar) which has a side chain including an
 CC aromatic group. They also need a penultimate C-terminal amino acid
 CC residue (Lip) with an alkyl side chain group, i.e. a 'LipAr' motif.
 CC Studies with these peptides have also shown that inhibiting peptides do
 CC not contain D-amino acids and that it is the presence of the ArLip motif
 CC that conveys effective betal integrin subunit dependent cell adhesion
 CC inhibition. The beta-1 integrin subunit dependent cell adhesion is
 CC important for cell adhesion to extracellular matrix proteins, and the
 CC subunit is expressed on tumours such as melanomas. Therefore these LipAr
 CC motif containing peptides may be important in the treatment of cancer.
 XX
 SQ Sequence 5 AA;

Query Match 78.1%; Score 25; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRARI 5
 |||||
 Db 1 PRARI 5

RESULT 6
 AAB19066
 ID AAB19066 standard; peptide; 5 AA.
 XX
 AC AAB19066;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of a betal-integrin inhibitor.
 XX
 KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
 KW central nervous system ischemic injury; myocardial infarction;

KW betal-integrin; stroke; surgical incision; injury-related trauma;
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX Synthetic.
 XX WO2000056350-A2.
 XX 28-SEP-2000.
 XX 22-MAR-2000; 2000WO-US07680.
 XX 22-MAR-1999; 99US-0125634.
 XX 24-NOV-1999; 99US-0167538.
 XX (MINU) UNIV MINNESOTA.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX (SENT-) SENTRON MEDICAL INC.
 XX McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
 XX Furcht LT;
 XX WPI; 2000-656062/63.
 XX Inhibition of inflammatory leukocyte mediated destruction of tissue in
 XX a patient, comprises administering a peptide inhibitor of
 XX betal-integrin, useful for treatment of e.g. cancer and osteoporosis -
 XX Claim 3; Page 38; 61pp; English.
 XX AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
 XX betal-integrin which is responsible for leukocyte mediated tissue
 XX destruction. The peptides are useful for inhibiting inflammatory
 XX leukocyte mediated destruction of tissue which occurs as a result of
 XX central nervous system (CNS) ischemic injury, myocardial infarction,
 XX angioplasty, surgical incisions, injury-related trauma, and/or
 XX transplant reperfusion, exposure to heat, cold, light, electricity
 XX and/or chemicals. They are also useful for the treatment of stroke, a
 XX burn type injury, cancer, and osteoporosis.
 XX Sequence 5 AA;
 XX Query Match 78.1%; Score 25; DB 21; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRARI 5
 DB 1 PRARI 5
 RESULT 7
 AAB19067
 ID AAB19067 standard; peptide; 5 AA.
 XX AAB19067;
 AC AAB19067;
 XX 08-FEB-2001 (first entry)
 DT 08-FEB-2001 (first entry)
 DE Amino acid sequence of a betal-integrin inhibitor.
 XX Betal-integrin inhibitor; leukocyte mediated tissue destruction;
 KW central nervous system ischemic injury; myocardial infarction;
 KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX Synthetic.
 OS Synthetic.
 XX WO2000056350-A2.
 XX 28-SEP-2000.
 XX 22-MAR-2000; 2000WO-US07680.

PR 22-MAR-1999; 99US-0125634.
 XX 24-NOV-1999; 99US-0167538.
 XX (MINU) UNIV MINNESOTA.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX (SENT-) SENTRON MEDICAL INC.
 XX McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
 XX Furcht LT;
 XX WPI; 2000-656062/63.
 XX Inhibition of inflammatory leukocyte mediated destruction of tissue in
 XX a patient, comprises administering a peptide inhibitor of
 XX betal-integrin, useful for treatment of e.g. cancer and osteoporosis -
 XX Claim 3; Page 38; 61pp; English.
 XX AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
 XX betal-integrin which is responsible for leukocyte mediated tissue
 XX destruction. The peptides are useful for inhibiting inflammatory
 XX leukocyte mediated destruction of tissue which occurs as a result of
 XX central nervous system (CNS) ischemic injury, myocardial infarction,
 XX angioplasty, surgical incisions, injury-related trauma, and/or
 XX transplant reperfusion, exposure to heat, cold, light, electricity
 XX and/or chemicals. They are also useful for the treatment of stroke, a
 XX burn type injury, cancer, and osteoporosis.
 XX Sequence 5 AA;
 XX Query Match 78.1%; Score 25; DB 21; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RARIY 6
 DB 1 RARIY 5
 RESULT 8
 AAY28513
 ID AAY28513 standard; peptide; 4 AA.
 XX AAY28513;
 AC AAY28513;
 XX 19-OCT-1999 (first entry)
 DT 19-OCT-1999 (first entry)
 DE Beta-1 integrin cell adhesion modulator analogue #26.
 XX Beta 1 integrin dependent cell adhesion; lipAr motif; tumour;
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX Synthetic.
 OS Synthetic.
 XX WO9937669-A1.
 XX 29-JUL-1999.
 DT 29-JUL-1999.
 DE 29-JUL-1999.
 XX 21-JAN-1999; 99WO-US01236.
 XX 12-AUG-1998; 98US-0096212.
 XX 22-JAN-1998; 98US-0072119.
 XX 12-AUG-1998; 98US-0096211.
 XX (MINU) UNIV MINNESOTA.
 XX Brienza A, Furcht LT, McCarthy JB;
 XX WPI; 1999-469112/39.
 XX New peptides modulating betal integrin subunit dependent cell
 XX adhesion, useful to study cell adhesion e.g. alpha4betal integrin
 XX dependent adhesion important in tumour cell biology

CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 67
 CC polynucleotides of the invention, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis
 CC or treatment of cancer, tumours, neurodegenerative disorders,
 CC developmental abnormalities and fetal deficiencies, blood disorders,
 CC leukemias, diseases of the immune system, autoimmune diseases, hepatic
 CC and renal disease, inflammation, allergies, ischemic shock, Alzheimer's
 CC and cognitive disorders, schizophrenia, restenosis, cardiovascular
 CC disorders, wound healing, stroke, arthritis, obesity, asthma, sepsis,
 CC acne, psoriasis, transplant rejection, metabolic disorders, infections
 CC and AIDS. The polypeptides are also useful for identifying their binding
 CC partners.

XX SQ Sequence 6 AA;

Query Match 59.4%; Score 19; DB 20; Length 6;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ARIV 6
 ||:|
 Db 1 ARVY 4

RESULT 11
 AAY21060
 ID AAY21060 standard; Protein: 5 AA.

XX AC AAY21060;

XX DT 22-JUL-1999 (first entry)

XX DE Human p53 cellular tumour antigen mutant protein fragment 7.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.

XX OS Synthetic.

OS Homo sapiens.

XX PN WO9845322-A2.

XX PD 15-OCT-1998.

XX PF 02-APR-1998; 98WO-IB00705.

XX PR 10-APR-1997; 97US-0043163.

XX PA (UYUT-) RIJKSUNIV UTRECHT.

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

XX PI Burbach JPH, Grosveld FG, Van Leeuwen FW;

XX WPI; 1998-609901/51.

DR N-PSDB; AAY75765.

XX Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 PT RNA

PS Disclosure; Figure 14; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease, II
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.

XX SQ Sequence 5 AA;

Query Match 56.2%; Score 18; DB 19; Length 5;

Best Local Similarity 75.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRAR 4
 ||:|
 Db 2 PRSR 5

RESULT 12
 AAW74620
 ID AAW74620 standard; peptide: 5 AA.

XX AC AAW74620;

XX DT 21-DEC-1998 (first entry)

XX DE Analogue of chymotrypsin-cleaved supAR peptide 7.

XX Human; urokinase receptor; UPAR; soluble UPAR; SUPAR; chymotrypsin;
 KW cleavage; cancer; autoimmune disease; inflammatory disorder;
 KW wound healing; antigen; vaccination; HIV.

XX OS Homo sapiens.

XX PN WO9842733-A1.

XX PD 01-OCT-1998.

XX PF 18-MAR-1998; 98WO-EP01547.

XX PR 20-MAR-1997; 97US-0041112.

XX PA (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.

PA (UYMI-) UNIV MILAN STUDI.

XX PI Blasi F, Fazioli F, Nicolai S, Resnati M;

XX WPI; 1998-531946/45.

XX New soluble urokinase receptor products obtained by chymotrypsin
 PT cleavage - useful for, e.g. treating cancers, autoimmune diseases
 PT and inflammatory disorders or for stimulating wound healing

XX Disclosure; Page 13; 59pp; English.

XX This is the nucleotide sequence of a functional analogue of the
 CC chymotrypsin-cleaved human soluble urokinase receptor (SUPAR)
 CC peptide used in the method of the invention. In this process SUPAR
 CC products obtained by chymotrypsin cleavage is used to treat cancer,

CC autoimmune disease, inflammatory disorders. SUPAR peptide or its
 CC functional peptide may be used for stimulating or increasing wound
 CC healing, stimulating the kinase activity. A peptide comprising the
 CC sequence SRGRY or its functional analogue may be used for stimulating
 CC or increasing, e.g. the chemotactic activity of a cell, a local
 CC inflammatory response and anti-tumour immunity in autologous bone
 CC marrow transplantation treatment of an individual, e.g. a human
 CC patient, who is immunodeficient. These products may also be used for
 CC increasing the immunogenicity of antigens in vaccination, e.g. against
 CC viral infections such as HIV infection.

XX
 SQ Sequence 5 AA;

Query Match 56.2%; Score 18; DB 19; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRAR 4
 ||:|
 Db 1 PRSR 4

RESULT 13
 AAEL11144
 ID AAEL11144 standard; peptide; 5 AA.
 AC AAEL11144;
 DT 18-DEC-2001 (first entry)
 XX Chymotryptic peptide #14 of phAB fusion protein.

DE Phenylalanine hydroxylase; PAH; phbA; 4a-carbinolamine dehydratase; phbB;
 KW aromatic aminotransferase; phbC; milk protein; animal protein; casein;
 KW proteinaceous food product; globulin; whey protein; phenylketonuria;
 KW PKU; inherited metabolic disorder; impaired brain function; nootropic;
 KW cell therapy; chymotryptic peptide.
 XX
 OS Unidentified.
 XX
 XX WO200168822-A2.
 XX
 XX 20-SEP-2001.
 XX
 XX 14-MAR-2001; 2001WO-DK00172.
 XX
 XX 14-MAR-2000; 2000US-0525116.
 XX
 XX (NILA-) NILAB APS.
 XX
 XX Johnsen M, Ravn P, Madsen SM, Vrang A, Israelsen H, Bredmose L;
 PI Arnau J, Jensen SH, Gjetting T, Nielsen E;
 XX
 XX WPI; 2001-590055/66.
 XX
 XX Novel recombinant cells comprising a nucleic acid encoding a gene
 PT product having phenylalanine hydroxylase activity, that is derived from
 PT a prokaryotic organism, is useful for treating phenylketonuria in
 PT mammals -
 XX
 XX Example 8; Page 48; 91pp; English.

CC The patent discloses novel cells comprising a nucleic acid encoding
 CC a gene product having phenylalanine hydroxylase (PAH) activity such
 CC as phenylalanine hydroxylase (phbA), 4a-carbinolamine dehydratase
 CC (phbB) and aromatic aminotransferase (phbC), which are derived
 CC from a prokaryotic organism. The patent also relates to fusion
 CC proteins comprising a protein enhancing and/or stabilising the
 CC PAH activity in addition to PAH activity. The cells are useful
 CC for producing PAH. The sequences of the invention are also useful
 CC for preparing a proteinaceous food product (animal protein such
 CC as a milk protein derived from casein, globulin or a whey protein)
 CC having reduced content of phenylalanine. The method involves contacting

CC the food product starting material with the cells or fusion proteins
 CC such that at least part of the phenylalanine content of the starting
 CC material is converted into compounds that do not cause phenylketonuria
 CC (PKU) by the enzymatically active product. PAH enzyme is useful for
 CC manufacturing a medicament for treating PKU, which is an inherited
 CC metabolic disorder resulting in an accumulation in the body of
 CC L-phenylalanine and metabolites that can cause impaired brain
 CC function. The present sequence is chymotryptic peptide of phAB fusion
 CC protein.

XX
 SQ Sequence 5 AA;

Query Match 56.2%; Score 18; DB 22; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ARYI 6
 ||:|
 Db 2 ARLY 5

RESULT 14
 AAEL24433
 ID AAEL24433 standard; peptide; 5 AA.
 XX
 AC AAEL24433;
 DT 04-OCT-2002 (first entry)
 XX
 DE Transporter peptide, T7.
 XX
 KW Transporter peptide; therapy; colon cancer; neurodegenerative disorder;
 KW diabetes; respiratory ailment; cardioplegia; viral infection; cytostatic;
 KW viricide; neuroprotective.
 XX
 OS Unidentified.
 XX
 XX WO200231109-A2.
 XX
 XX 18-APR-2002.
 XX
 XX 15-OCT-2001; 2001WO-IB02423.
 XX
 XX 13-OCT-2000; 2000US-240315P.
 XX
 XX (UYLA-) UNIV LAUSANNE.
 XX
 XX Bonny C;
 XX
 XX WPI; 2002-479626/51.
 XX
 XX Novel transporter peptide useful for the intracellular delivery of
 PT biological effectors for treating diabetes, colon cancer, respiratory
 PT ailments, neurodegenerative disorders, cardioplegia, and viral
 PT infections -
 XX
 XX Claim 35; Page 26; 50pp; English.

CC The present invention relates to novel transporter peptides with the
 CC capacity to facilitate transport of an effector across a biological
 CC membrane. Sequences of the invention are useful for translocating an
 CC effector into the cytoplasm and nucleus of a eukaryotic cell preferably
 CC a human cell. They are also useful for increasing the intracellular
 CC concentration of an effector within a eukaryotic cell, preferably human
 CC cell. Transporter peptides of the invention are useful for transporting
 CC an effector across a biological membrane, for targeting various cell
 CC types for the intracellular delivery of drugs and therapeutic agents
 CC and for increasing the biological activity of the effector to which
 CC it is coupled. Pharmaceutical compositions comprising the transporter
 CC peptides are useful for treating or preventing diseases such as colon
 CC cancer, diabetes, respiratory ailments, neurodegenerative disorders,
 CC cardioplegia and viral infections. The present sequence is a transporter
 CC peptide of the invention. This peptide can be translocated across a

CC membrane of lung cells.

Job time : 33.4 secs

XX SQ Sequence 5 AA;

Query Match 56.2%; Score 18; DB 23; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PRAR 4
||:
Db 1 PRSR 4

RESULT 15

AAP50198
ID AAP50198 standard; peptide; 5 AA.

XX AC AAP50198;

XX DT 17-OCT-1991 (first entry)

XX DE Sequence of oligopeptide 1 specific to the beta-subunit of human
XX DE chorionic gonadotropin (HCG).

XX KW Contraception; assay; pregnancy test; luteinising hormone;
XX KW human chorionic gonadotropin.

XX OS Homo sapiens.

XX PN EP142387-A.

XX PD 22-MAY-1985.

XX PF 23-AUG-1984; 84EP-0401710.

XX PR 26-AUG-1983; 83EP-0401714.

XX PR 23-AUG-1984; 84EP-0401710.

XX PA (ANDA-) ANDA BIOLOGICALS.

XX PI Maes RF;

XX DR WPI; 1985-124152/21.

XX PT Prepn. of anti-HCG and anti-LH vaccines - by use of
XX PT oligo-peptide(s) specific to beta-sub-unit of LH and HCG

XX PS Claim 1; Page 17; 22pp; English.

XX CC Oligopeptides AAP50198-P50205, specific to the beta-subunit of LH and
XX CC of HCG, located near cysteine groups, are used in a claimed process
XX CC for the preparation of anti-HCG and anti-LH vaccines. The vaccines
XX CC are characterised in that these oligopeptides are complexed upon
XX CC themselves and between themselves by disulphur bridges, upon their
XX CC own beta-subunit of HCG and LH or upon oligopeptides containing
XX CC cysteine whose AA chain is common to LH and HCG, namely the peptides
XX CC in AAP50208-P50212. Through sulphur bridges the specific oligopeptides
XX CC are administered by injection in vaccines to cause prodn. of
XX CC antibodies so that a contraceptive effect is achieved; and the
XX CC antibodies are also useful in assays for HCG and LH in body fluids.

XX SQ Sequence 5 AA;

Query Match 53.1%; Score 17; DB 6; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 PRAR 4
||:
Db 1 PRCR 4

Search completed: December 12, 2002, 15:17:15

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Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:15:23 : Search time 11.4 seconds
(without alignments)
15.486 Million cell updates/sec

Title: US-09-600-432-24

Perfect score: 32

Sequence: 1 PRARIY 6

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 32749

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
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- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Printed No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	25	78.1	5	4	US-09-101-751A-57
2	18	56.2	4	2	US-08-480-133A-15
3	18	56.2	4	3	US-09-008-308-30
4	18	56.2	5	4	US-09-381-244B-13
5	17	53.1	5	1	US-08-375-879-4
6	17	53.1	5	3	US-09-125-517A-42
7	17	53.1	5	4	US-09-284-625-6
8	17	53.1	5	4	US-09-381-244B-15
9	17	53.1	6	2	US-08-616-669A-57
10	17	53.1	6	3	US-09-125-517A-8
11	17	53.1	6	4	US-09-326-440-57
12	17	53.1	6	4	US-08-057-052-7
13	16	50.0	4	1	US-08-240-514-5
14	16	50.0	4	2	US-08-612-302A-5
15	16	50.0	4	2	US-08-637-759B-421
16	16	50.0	4	2	US-08-232-539D-46
17	16	50.0	4	3	US-08-871-355A-421
18	16	50.0	4	3	US-08-466-151-59
19	16	50.0	4	3	US-09-008-308-29
20	16	50.0	4	4	US-08-974-549A-541
21	16	50.0	4	4	US-08-466-163B-59
22	16	50.0	4	4	US-09-201-945-421
23	16	50.0	5	1	US-08-095-162-22
24	16	50.0	5	1	US-08-021-608D-21
25	16	50.0	5	1	US-08-470-220A-22
26	16	50.0	5	1	US-08-458-997-2
27	16	50.0	5	1	US-08-726-160-21

28	16	50.0	5	1	US-07-923-724-19	Sequence 19, Appl
29	16	50.0	5	2	US-08-609-426A-19	Sequence 19, Appl
30	16	50.0	5	2	US-08-374-652C-11	Sequence 11, Appl
31	16	50.0	5	3	US-08-967-374-22	Sequence 22, Appl
32	16	50.0	5	3	US-08-208-264A-36	Sequence 36, Appl
33	16	50.0	5	3	US-09-008-308-9	Sequence 9, Appl
34	16	50.0	5	4	US-09-421-097-36	Sequence 36, Appl
35	16	50.0	5	4	US-09-505-931-22	Sequence 22, Appl
36	16	50.0	6	1	US-07-859-281C-18	Sequence 18, Appl
37	16	50.0	6	1	US-08-022-381A-19	Sequence 19, Appl
38	16	50.0	6	1	US-08-049-195A-2	Sequence 2, Appl
39	16	50.0	6	1	US-08-475-827A-19	Sequence 19, Appl
40	16	50.0	6	1	US-08-704-170-89	Sequence 89, Appl
41	16	50.0	6	1	US-08-458-997-3	Sequence 3, Appl
42	16	50.0	6	1	US-08-458-997-5	Sequence 5, Appl
43	16	50.0	6	1	US-08-458-997-8	Sequence 8, Appl
44	16	50.0	6	1	US-08-458-997-9	Sequence 9, Appl
45	16	50.0	6	1	US-08-458-997-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-101-751A-57
; Sequence 57, Application US/09101751A
; Patent No. 6465253
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS
; FILE REFERENCE: 85710
; CURRENT APPLICATION NUMBER: US/09/101,751A
; PRIOR FILING DATE: 1999-01-29
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (..)
; OTHER INFORMATION: Description of Unknown Organism: Artificial
; OTHER INFORMATION: Sequence
US-09-101-751A-57

Query Match 78.1% Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 PRARI 5

DB 1 PRARI 5

RESULT 2
US-08-480-133A-15
; Sequence 15, Application US/08480133A
; Patent No. 5840691
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: McCarthy, James B.
; APPLICANT: Wahl, Sharon M.

```
; APPLICANT: Allen, Janice B.
; APPLICANT: Billups, Kevin L.
; APPLICANT: Everett, Jeffrey E.
; TITLE OF INVENTION: Method for Treating Inflammatory
; TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5840691west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,133A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,903
; FILING DATE: 21-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,296
; FILING DATE: 10-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 600-308US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-480-133A-15

Query Match 56.2%; Score 18; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RARI 5
Db 1 RARI 4

RESULT 3
US-09-008-308-30
; Sequence 30, Application US/09008308
; Patent No. 6080575
; GENERAL INFORMATION:
; APPLICANT: Heitmann, Hans H.
; APPLICANT: Mueller, Rolf
; APPLICANT: Sedlacek, Hans-Harald
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
; TITLE OF INVENTION: ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES, AND
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,308
; FILING DATE: 16-JAN-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197 01 141.1
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-09-008-308-30

Query Match 56.2%; Score 18; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RARI 5
Db 1 RARI 4

RESULT 4
US-09-381-244B-13
; Sequence 13, Application US/09381244B
; Patent No. 6462170
; GENERAL INFORMATION:
; APPLICANT: BLASI, Francesco
; APPLICANT: FAZIOLI, Francesca
; APPLICANT: RESNATI, Massimo
; APPLICANT: NICOLAI, Sidenius
; TITLE OF INVENTION: uPAR Mimicking Peptide
; FILE REFERENCE: 0471-0143P
; CURRENT APPLICATION NUMBER: US/09/381,244B
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/EP98/01547
; PRIOR FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: peptide analogue of the human uPAR
; US-09-381-244B-13

Query Match 56.2%; Score 18; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRAR 4
Db 1 PRSR 4

RESULT 5
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US-08-375-879-4
; Sequence 4, Application US/08375879
; Patent No. 5614608
; GENERAL INFORMATION:
; APPLICANT: Krchnak, Viktor
; APPLICANT: Lebl, Michal
; APPLICANT: Seligman, Bruce
; TITLE OF INVENTION: Apparatus and Method for Multiple
; TITLE OF INVENTION: Synthesis of Organic Compounds on Polymer Support
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/375,879
; FILING DATE: 20-JAN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18872
; REFERENCE/DOCKET NUMBER: 7156-068
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-375-879-4

Query Match 53.1%; Score 17; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRAR 4
Db 2 PRGR 5

RESULT 6
US-09-125-517A-42
; Sequence 42, Application US/09125517A
; Patent No. 6087336
; GENERAL INFORMATION:
; APPLICANT: Cotton, Ronald
; APPLICANT: Edwards, Philip Neil
; APPLICANT: Luke, Richard William Arthur
; TITLE OF INVENTION: Peptide Derivatives
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth St., N.W., Suite 701 East
; CITY: Tower
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE: 20-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9603855.9
; FILING DATE: 23-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9620819.4
; FILING DATE: 05-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1991-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-125-517A-42

Query Match 53.1%; Score 17; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
Db 2 RARV 5

RESULT 7
US-09-284-625-6
; Sequence 6, Application US/09284625
; Patent No. 6207644
; GENERAL INFORMATION:
; APPLICANT: Luke, Richard William
; APPLICANT: Cotton, Richard
; TITLE OF INVENTION: Peptide Analogues Containing a 7-membered Lactam Ring
; FILE REFERENCE: 1991-169
; CURRENT APPLICATION NUMBER: US/09/284,625
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: PCT/GB97/02837
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: GB 96218367
; PRIOR FILING DATE: 1996-10-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PPT
; ORGANISM: Homo sapiens
; US-09-284-625-6

Query Match 53.1%; Score 17; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
Db 2 RARV 5

RESULT 8
US-09-381-244B-15
; Sequence 15, Application US/09381244B
; Patent No. 6462170

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;
; GENERAL INFORMATION:
; APPLICANT: BLASI, Francesco
; APPLICANT: FAZIOLI, Francesca
; APPLICANT: RESNATI, Massimo
; APPLICANT: NICOLAI, Sidenius
; TITLE OF INVENTION: upar Mimicking Peptide
; FILE REFERENCE: 0471-0143P
; CURRENT APPLICATION NUMBER: US/09/381,244B
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/EP98/01547
; PRIOR FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: peptide analogue of the human upar
US-09-381-244B-15

Query Match 53.1%; Score 17; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 PRAR 4
| | |
Db 1 PRGR 4

RESULT 9
US-08-616-669A-57
; Sequence 57, Application US/08616669A
; Patent No. 5948765
; GENERAL INFORMATION:
; APPLICANT: Muslim, Anthony J.
; APPLICANT: Shaw, Andrew S.
; TITLE OF INVENTION: Inhibition of Intracellular Signal
; TITLE OF INVENTION: Transduction by 14-3-3-Binding Peptides
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Boulevard, Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: US
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/616.669A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Holland, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 964064
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site

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; LOCATION: 4
; OTHER INFORMATION: /note= "A phosphorylated serine"
US-08-616-669A-57

Query Match 53.1%; Score 17; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RARIY 6
| : | |
Db 1 RSRXY 5
| : | |

RESULT 10
US-09-125-517A-8
; Sequence 8, Application US/09125517A
; Patent No. 6087336
; GENERAL INFORMATION:
; APPLICANT: Cotton, Ronald
; APPLICANT: Edwards, Philip Neil
; APPLICANT: Luke, Richard William Arthur
; TITLE OF INVENTION: Peptide Derivatives
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth St., N.W., Suite 701 East
; CITY: Tower
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/125,517A
; APPLICATION NUMBER: GB 9603855.9
; FILING DATE: 20-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; FILING DATE: 23-FEB-1996
; APPLICATION NUMBER: GB 9620819.4
; FILING DATE: 05-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1991-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "5-Phenylpentanoyl-Ala"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 6
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note=
; OTHER INFORMATION: "[(S)-2-((R)-3-amino-2-oxopyrrolidin-1-yl)propanoyl]-Gly-4
US-09-125-517A-8

Query Match 53.1%; Score 17; DB 3; Length 6;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
 Db 2 RARV 5

RESULT 11
 US-09-326-440-57
 ; Sequence 57, Application US/09326440
 ; Patent No. 6207393
 ; GENERAL INFORMATION:
 ; APPLICANT: Muslin, Anthony J.
 ; APPLICANT: Shaw, Andrew S.
 ; TITLE OF INVENTION: Inhibition of Intracellular Signal
 ; TITLE OF INVENTION: Transduction by 14-3-3-Binding Peptides
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howell & Haferkamp, L.C.
 ; STREET: 7733 Forsyth Boulevard, Suite 1400
 ; CITY: St. Louis
 ; STATE: MO
 ; COUNTRY: US
 ; ZIP: 63105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/326,440
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/616,669
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Holland, Donald R.
 ; REGISTRATION NUMBER: 35,197
 ; REFERENCE/DOCKET NUMBER: 964064
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314) 727-5188
 ; TELEFAX: (314) 727-6092
 ; INFORMATION FOR SEQ ID NO: 57:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 4
 ; OTHER INFORMATION: /note= "A phosphorylated serine"
 ; US-09-326-440-57

Query Match 53.1%; Score 17; DB 4; Length 6;
 Best Local Similarity 60.0%; Pred. No. 1.9e+05;
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QY 2 RARIY 6
 Db 1 RSRXY 5

RESULT 12
 US-09-057-052-7
 ; Sequence 7, Application US/09057052
 ; Patent No. 6331422
 ; GENERAL INFORMATION:
 ; APPLICANT: Hubbell, Jeffrey A.

APPLICANT: Schense, Jason
 TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for
 Tissue Engineering
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Vinson & Elkins L.L.P.
 STREET: 600 Congress Avenue, Suite 2700
 CITY: Austin
 STATE: Texas
 COUNTRY: US
 ZIP: 78701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/057,052
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/042,143
 FILING DATE: 03-APR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mayfield, Denise L.
 REGISTRATION NUMBER: 33,732
 REFERENCE/DOCKET NUMBER: CAL430.23000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 495-8400
 TELEFAX: (512) 495-8612
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-09-057-052-7

Query Match 53.1%; Score 17; DB 4; Length 6;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
 Db 3 RARV 6

RESULT 13
 US-08-240-514-5
 ; Sequence 5, Application US/08240514
 ; Patent No. 5670347
 ; GENERAL INFORMATION:
 ; APPLICANT: GOPAL, T. Venkat
 ; TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/240,514
 FILING DATE: 11-MAY-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.

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; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 73521/102/CLIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-240-514-5

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Query Match 50.0%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0;

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Qy 1 PRAR 4
Db 1 PRKR 4

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RESULT 14
US-08-612-302A-5
; Sequence 5, Application US/08612302A
; Patent No. 5811297
; Patent No. 5811297 5780297
; GENERAL INFORMATION:
; APPLICANT: GOPAL, T. Venkat
; TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: One Westlakes, Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,302A
; FILING DATE: 7 March 1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: AMBA-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 407-0700
; TELEFAX: (610) 407-0701
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; US-08-612-302A-5

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Query Match 50.0%; Score 16; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0;

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Qy 1 PRAR 4
Db 1 PRKR 4

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RESULT 15
US-08-637-759B-421
; Sequence 421, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 421:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-637-759B-421

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Query Match 50.0%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 PRA 3
Db 2 PRA 4

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Job time : 12.4 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2002, 15:17:24 ; Search time 6.3 Seconds
(without alignments)
15.869 Million cell updates/sec

Title: US-09-600-432-24
Perfect score: 32
Sequence: 1 PRARIY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105981 seqs, 16662342 residues

Total number of hits satisfying chosen parameters: 5573

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:*

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3:	/cgn2.6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	56.2	4	10	US-09-010-714-10
2	18	56.2	5	10	US-09-977-831-30
3	17	53.1	6	9	US-10-024-918-7
4	17	53.1	6	10	US-09-887-469-20
5	16	50.0	4	8	US-08-484-409-24
6	16	50.0	4	10	US-09-802-077-59
7	16	50.0	4	10	US-09-802-096-59
8	16	50.0	6	10	US-09-802-077-21
9	16	50.0	6	10	US-09-802-077-38
10	16	50.0	6	10	US-09-802-096-21
11	16	50.0	6	10	US-09-802-096-38
12	16	50.0	6	12	US-10-036-418-17
13	16	50.0	6	12	US-10-036-418-18
14	15	46.9	4	9	US-09-900-936-10
15	15	46.9	4	10	US-09-771-192-10
16	15	46.9	4	10	US-09-837-697A-10
17	15	46.9	5	9	US-09-900-936-9
18	15	46.9	5	10	US-09-771-192-9
19	15	46.9	5	10	US-09-837-697A-9

20	15	46.9	6	9	US-09-900-936-5	Sequence 5, Appli
21	15	46.9	6	9	US-09-900-936-8	Sequence 8, Appli
22	15	46.9	6	10	US-09-771-192-5	Sequence 5, Appli
23	15	46.9	6	10	US-09-771-192-8	Sequence 8, Appli
24	15	46.9	6	10	US-09-837-697A-5	Sequence 5, Appli
25	15	46.9	6	10	US-09-837-697A-8	Sequence 8, Appli
26	15	46.9	6	12	US-10-066-151-5	Sequence 5, Appli
27	14	43.8	5	10	US-09-800-433-5	Sequence 5, Appli
28	14	43.8	5	10	US-09-800-433-7	Sequence 7, Appli
29	14	43.8	5	10	US-09-977-831-19	Sequence 19, Appli
30	14	43.8	5	10	US-09-947-387-47	Sequence 47, Appli
31	14	43.8	6	9	US-09-823-823-66	Sequence 66, Appli
32	14	43.8	6	10	US-09-904-599A-3	Sequence 3, Appli
33	14	43.8	6	10	US-09-823-829-66	Sequence 66, Appli
34	14	43.8	6	12	US-10-066-151-6	Sequence 6, Appli
35	13	40.6	4	8	US-08-484-409-31	Sequence 31, Appli
36	13	40.6	4	12	US-10-041-030-25	Sequence 25, Appli
37	13	40.6	5	9	US-10-104-019-43	Sequence 43, Appli
38	13	40.6	5	10	US-09-803-126-18	Sequence 18, Appli
39	13	40.6	5	10	US-09-953-657-4	GENERAL INFORMA
40	13	40.6	5	10	US-09-748-114-28	Sequence 28, Appli
41	13	40.6	6	10	US-09-113-696B-21	Sequence 21, Appli
42	13	40.6	6	10	US-09-808-832-17	Sequence 17, Appli
43	13	40.6	6	10	US-09-808-832-89	Sequence 89, Appli
44	13	40.6	6	10	US-09-808-387-45	Sequence 45, Appli
45	12	37.5	4	9	US-09-984-333-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-010-714-10
; Sequence 10, Application US/09010714
; Patent No. US20020012942A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; APPLICANT: Iida, Joji
; TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
; FILE REFERENCE: 600.332US01
; CURRENT APPLICATION NUMBER: US/09/010,714
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-010-714-10

Query Match 56.2%; Score 18; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RARI 5
Db 1 RARI 4

RESULT 2
US-09-977-831-30
; Sequence 30, Application US/09977831
; Patent No. US20020120100A1
; GENERAL INFORMATION:
; APPLICANT: PACT, Tech Transfer Office University of Lausanne
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 transporter peptides
; CURRENT APPLICATION NUMBER: US/09/977,831
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/240,315

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; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-09-977-831-30

Query Match          56.2%; Score 18; DB 10; Length 5;
Best Local Similarity 75.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRAR 4
Db 1 PRSR 4

RESULT 3
US-10-024-918-7
; Sequence 7, Application US/10024918
; Patent No. US20020168718A1
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey
; APPLICANT: Schense, Jason
; APPLICANT: Zisch, Andreas
; APPLICANT: Hall, Heike
; TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
; FILE REFERENCE: CIT 2606 CIP
; CURRENT APPLICATION NUMBER: US/10/024,918
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heparin-binding sequence from fibronectin
US-10-024-918-7

Query Match          53.1%; Score 17; DB 9; Length 6;
Best Local Similarity 75.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
Db 3 RARV 6

RESULT 4
US-09-887-469-20
; Sequence 20, Application US/09887469
; Patent No. US20020146433A1
; GENERAL INFORMATION:
; APPLICANT: Kremp, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; FILE REFERENCE: 15280-424-1US
; CURRENT APPLICATION NUMBER: US/09/887,469
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20

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; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Respiratory Syncytial Virus
US-09-887-469-20

Query Match          53.1%; Score 17; DB 10; Length 6;
Best Local Similarity 75.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
Db 1 RARV 4

RESULT 5
US-08-484-409-24
; Sequence 24, Application US/08484409
; Patent No. US20020076412A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Zamvil, Scott
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,409
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.409C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-484-409-24

Query Match          50.0%; Score 16; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RIV 6
Db 1 RIV 3

RESULT 6
US-09-802-077-59
; Sequence 59, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.

```


; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 59
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-59

Query Match 50.0%; Score 16; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRA 3
|||
Db 1 PRA 3

RESULT 7

US-09-802-096-59
; Sequence 59, Application US/09802096
; Patent No. US2001003839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 59
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-59

Query Match 50.0%; Score 16; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRA 3
|||
Db 1 PRA 3

RESULT 8

US-09-802-077-21
; Sequence 21, Application US/09802077
; Patent No. US2001003842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-21

Query Match 50.0%; Score 16; DB 10; Length 6;
Best Local Similarity 50.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PRARIY 6
|||
Db 1 PREQQY 6

RESULT 9

US-09-802-077-38
; Sequence 38, Application US/09802077
; Patent No. US2001003842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-38

Query Match 50.0%; Score 16; DB 10; Length 6;
Best Local Similarity 50.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PRARIY 6
|||
Db 1 PREQQY 6

RESULT 10

US-09-802-096-21
; Sequence 21, Application US/09802096
; Patent No. US2001003839A1
; GENERAL INFORMATION:

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; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-21

Query Match          50.0%; Score 16; DB 10; Length 6;
Best Local Similarity 50.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PRARI 6
Db 1 PREQY 6

RESULT 11
US-09-802-096-38
; Sequence 38, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-38

Query Match          50.0%; Score 16; DB 10; Length 6;
Best Local Similarity 50.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PRARI 6
Db 1 PREQY 6

RESULT 12
US-10-036-418-17
; Sequence 17, Application US/10036418
; Patent No. US20020127624A1
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; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INGap Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetus
US-10-036-418-17

Query Match          50.0%; Score 16; DB 12; Length 6;
Best Local Similarity 60.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PRARI 5
Db 2 PSSRI 6

RESULT 13
US-10-036-418-18
; Sequence 18, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INGap Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetus
US-10-036-418-18

Query Match          50.0%; Score 16; DB 12; Length 6;
Best Local Similarity 60.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PRARI 5
Db 1 PSSRI 5

RESULT 14
US-09-900-936-10
; Sequence 10, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: Gierrega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-4)
US-09-900-936-10

Query Match      46.9%; Score 15; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 RY 6
   | |
DB 2 RY 4

RESULT 15
US-09-771-192-10
; Sequence 10, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizegda, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-4)
US-09-771-192-10

Query Match      46.9%; Score 15; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 RY 6
   | |
DB 2 RY 4

```

Search completed: December 12, 2002, 15:21:20
Job time : 6.3 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:58 ; Search time 13.2 Seconds
(without alignments)
43.697 Million cell updates/sec

Title: US-09-600-432-24

Perfect score: 32

Sequence: 1 PRARIY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	13	40.6	5	2 S62883	seminal plasma pro
2	12	37.5	4	2 A02147	phagocytosis-stimu
3	12	37.5	5	2 B22565	R-phycocerythrin al
4	12	37.5	6	2 PT0618	T-cell receptor be
5	11	34.4	4	2 PT0721	peptidyl-di-peptida
6	11	34.4	5	2 JN0860	phytosulfo kinase alp
7	11	34.4	5	3 JT0870	peptidyl-di-peptida
8	10	31.2	6	2 JN0861	pyruvate kinase (E
9	10	31.2	6	2 A11490	laminin B1 - weste
10	10	31.2	6	2 I49421	orf 3 tara 5'-regi
11	10	31.2	6	4 S15596	protamine p1 - ora
12	9	28.1	4	2 I61883	protamine p1 - Cer
13	9	28.1	4	2 I84439	protamine p1 - sav
14	9	28.1	5	2 C41225	copper resistance
15	9	28.1	5	2 I40702	primase - Citrobac
16	9	28.1	5	2 I39964	ribosomal protein
17	9	28.1	5	2 I39966	ribosomal protein
18	9	28.1	5	2 I39965	ribosomal protein
19	9	28.1	5	2 P00009	angiotensin-conver
20	9	28.1	6	2 PC4127	hypothetical 6 pro
21	9	28.1	6	2 P60110	repetitive protein
22	9	28.1	6	2 A61140	sperm acrosomal pr
23	9	28.1	6	2 I37027	protamine p1 - gor
24	9	28.1	6	2 B33932	Ig mu chain D regi
25	9	28.1	6	2 PT0518	T-cell receptor be
26	9	28.1	6	2 PT0568	T-cell receptor be
27	8	25.0	6	2 S11556	hydrogensulfite re
28	8	25.0	6	2 A37765	hypothetical prote
29	8	25.0	6	2 A37765	hypothetical prote

30 8 25.0 6 2 A19780 transferrin - bovi
31 7 21.9 3 3 RHDTDO thyroliberin - Bom
32 7 21.9 3 3 RHFTG thyroliberin - pig
33 7 21.9 3 3 RHSGT thyroliberin - she
34 7 21.9 3 3 A92971 thyroliberin - eas
35 7 21.9 3 3 A33802 thvrotropin-releas
36 7 21.9 3 3 A22565 R-phycocerythrin al
37 7 21.9 3 3 A43391 TRH-like tripeptid
38 7 21.9 3 3 I78890 tyrosine protein k
39 7 21.9 3 3 S68328 blood cell protein
40 7 21.9 4 2 A30339 tyrosine-melanocyt
41 7 21.9 4 2 PL0140 carbon-monoxide de
42 7 21.9 4 2 A37832 phenol 2-monooxyge
43 7 21.9 4 2 S09478 globulin IV alpha
44 7 21.9 4 2 S53508 starvation-induced
45 7 21.9 4 2 S17255 ribosomal protein

ALIGNMENTS

RESULT 1

S62883

seminal plasma protein II - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S62883

R:Romero, A.; Varela, P.F.; Sanz, L.; Toepfer-Petersen, E.; Calvete, J.J.

FEBS Lett. 382, 15-17, 1996

A:Title: Crystallization and preliminary X-ray diffraction analysis of boar seminal p

A:Reference number: S62882; MUID:96196555; PMID:8612739

A:Accession: S62883

A:Molecule type: protein

A:Residues: 1-5 <ROW>

C:Complex: heterodimer; seminal plasma protein I and seminal plasma protein II

C:Keywords: glycoprotein; heterodimer; semen

Query Match 40.6%; Score 13; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ARI 5

Db 1 ARI 3

RESULT 2

A02147

phagocytosis-stimulating peptide (tuftsin) - human

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 03-Feb-1994

C:Accession: A02147

R:Nishioka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.

Biochem. Biophys. Res. Commun. 47, 172-179, 1972

A:Title: The characteristics, isolation and synthesis of the phagocytosis stimulating

A:Reference number: A02147; MUID:72187087; PMID:4112769

A:Accession: A02147

A:Molecule type: protein

A:Residues: 1-4 <NIS>

A:Note: a peptide having the same structure, physical properties, and biological acti

R:Fidalgo, B.V.; Najjar, V.A.

Biochemistry 6, 3386-3392, 1967

A:Reference number: A37502; MUID:68091045; PMID:4169272

A:Contents: annotation; immunoglobulin class

C:Comment: An IgG (called leucokinin) binds reversibly to the cell membrane of neutro

n is essential for maximum stimulation of the phagocytic activity of neutrophils.

C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 37.5%; Score 12; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PR 2

```

Db          3 PR 4
||
RESULT 3
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: B22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:95182601; PMID:3886644
A:Accession: B22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match      37.5%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PR 2
||
Db 4 PR 5
||
RESULT 4
PT0618
T-cell receptor beta chain V-D-J region (120-2CK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0618
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0618
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      37.5%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PR 2
||
Db 4 PR 5
||
RESULT 5
PT0721
T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0721
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0721
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      34.4%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 ARI 5
||
Db 1 ARL 3
||
RESULT 6
JN0860
peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito
C:Species: Sarda orientalis (striped bonito)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: JN0860
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory
A:Reference number: JN0859; MUID:94080036; PMID:7764272
A:Accession: JN0860
A:Molecule type: protein
A:Residues: 1-5 <MAT>
A:Experimental source: intestine
C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match      34.4%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRA 3
||
Db 3 PHA 5
||
RESULT 7
JT0870
phytosulfoxine alpha - garden asparagus (fragment)
C:Species: Asparagus officinalis (garden asparagus)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 19-Apr-2002
C:Accession: JT0870
R:Matsumura, Y.; Sakagami, Y.
Proc. Natl. Acad. Sci. U.S.A. 93, 7623-7627, 1996
A:Title: Phytosulfoxine, sulfated peptides that induce the proliferation of single me
A:Reference number: JT0870
A:Accession: JT0870
A:Molecule type: protein
A:Residues: 1-5 <MAT>

Query Match      34.4%; Score 11; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IY 6
||
Db 2 IY 3
||
RESULT 8
JN0861
peptidyl-dipeptidase A inhibitory peptide C111 - striped bonito
C:Species: Sarda orientalis (striped bonito)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: JN0861
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory
A:Reference number: JN0859; MUID:94080036; PMID:7764272
A:Accession: JN0861
A:Molecule type: protein
A:Residues: 1-6 <MAT>
A:Experimental source: liver
C:Comment: The carboxyl end is essential for the protein's expression of angiotensin
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor

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Query Match 31.2%; Score 10; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IX 6
 :
 Db 2 VY 3

RESULT 9

Al1490
 pyruvate kinase (EC 2.7.1.40) - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Mar-1995
 C:Accession: Al1490
 R:Hjelmquist, G.; Andersson, J.; Edlund, B.; Engstrom, L.
 Biochem. Biophys. Res. Commun. 61, 559-563, 1974
 A:Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate kinase p1
 A:Reference number: Al1490; MUID:75127438; PMID:4375989
 A:Accession: Al1490
 A:Molecule type: protein
 A:Residues: 1-6 <HJE>
 A:Experimental source: liver
 C:Keywords: glycolysis; phosphotransferase

Query Match 31.2%; Score 10; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RARI 5
 :
 Db 3 RASL 6

RESULT 10

I49421
 laminin B1 - western wild mouse (fragment)
 C:Species: Mus spretus (western wild mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I49421
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maizaki, Y.; Nadeau, J.H.
 Mamm. Genome 5, 349-355, 1994
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A:Reference number: I48334; MUID:94319082; PMID:8043949
 A:Accession: I49421
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6 <RES>
 A:Cross-references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829

Query Match 31.2%; Score 10; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IX 6
 :
 Db 1 VY 2

RESULT 11

SI5596
 orf 3 rara 5'-region - human
 C:Species: Homo sapiens (man)
 C>Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
 C:Accession: SI5596
 R:Brand, N.J.; Petkovich, M.; Chambon, P.
 Nucleic Acids Res. 18, 6799-6806, 1990
 A:Title: Characterization of a functional promoter for the human retinoic acid receptor-
 A:Reference number: SI5594; MUID:91088249; PMID:2175878
 A:Accession: SI5596
 A:Molecule type: DNA
 A:Residues: 1-6 <BRA>

A:Cross-references: EMBL:X56058; NID:g35876
 A>Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0
 C:Comment: This sequence is not thought to be translated.

C:Genetics:

A:Gene: GDB:RARA

A:Cross-references: GDB:I20337; OMIM:180240

A:Map position: 17q12-17q12

Query Match 31.2%; Score 10; DB 4; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRA 3
 :
 Db 3 PSA 5

RESULT 12

I61883
 protamine p1 - orangutan (fragment)
 C:Species: Pongo pygmaeus (orangutan)
 C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
 C:Accession: I61883
 R:Queralt, R.; Oliva, R.
 Gene 133, 197-204, 1993
 A:Title: Identification of conserved potential regulatory sequences of the protamine-
 A:Reference number: I37013; MUID:94040810; PMID:8224908
 A:Accession: I61883
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-4 <RES>
 A:Cross-references: EMBL:Z12146; NID:g38156; PIDN:CAA78130.1; PID:g4379372

Query Match 28.1%; Score 9; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AR 4
 :
 Db 2 AR 3

RESULT 13

I37013
 protamine p1 - Cercopithecus patas (fragment)
 C:Species: Cercopithecus patas
 C>Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
 C:Accession: I37013
 R:Queralt, R.; Oliva, R.
 Gene 133, 197-204, 1993
 A:Title: Identification of conserved potential regulatory sequences of the protamine-
 A:Reference number: I37013; MUID:94040810; PMID:8224908
 A:Accession: I37013
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-4 <RES>
 A:Cross-references: EMBL:Z12150; NID:g22814; PIDN:CAA78134.1; PID:g4377415

Query Match 28.1%; Score 9; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AR 4
 :
 Db 2 AR 3

RESULT 14

I84439
 protamine p1 - savannah baboon (fragment)
 C:Species: Papio hamadryas doguera (savannah baboon)
 C>Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
 C:Accession: I84439

R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810; PMID:8224908
A:Accession: I84439
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12147; MID:g38134; PIDN:CAA78131.1; PID:g4379349

Query Match 28.1%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AR 4
| |
Db 2 AR 3

RESULT 15
C41225
copper resistance protein - Pseudomonas syringae pv. tomato (fragment)
C:Species: Pseudomonas syringae pv. tomato
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C:Accession: C41225
R:Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem
A:Reference number: A41225; MUID:92020961; PMID:1924351
A:Accession: C41225
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <CHA>

Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PR 2
| |
Db 2 PK 3

Search completed: December 12, 2002, 15:20:08
Job time : 14.2 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:38 ; Search time 7.2 seconds
(without alignments)
34.564 Million cell updates/sec

Title: US-09-600-432-24
Perfect score: 32
Sequence: 1 PRARIY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	37.5	4	1 TUFT_HUMAN	P01858 homo sapien
2	11	34.4	5	1 PSK_DAUCA	P58261 daucus caro
3	9	28.1	4	1 FYRI_ATEL	P58706 anthopleura
4	8	25.0	6	1 UN06_CLOPA	P01351 clostridium
5	7	21.9	3	1 THYL_PIG	P01151 sus scrofa
6	7	21.9	4	1 DCM_L_PSECH	P19916 pseudomonas
7	7	21.9	4	1 FAR3_HIRME	P42562 hirudo medi
8	7	21.9	4	1 FAR4_HIRME	P42563 hirudo medi
9	7	21.9	4	1 RM01_YEAST	P36515 saccharomyc
10	7	21.9	5	1 AL14_CARMA	P81817 carlinus ma
11	7	21.9	5	1 BPP7_BOTIN	P30425 bothrops in
12	7	21.9	5	1 EI03_LITRU	P82099 litoria rub
13	7	21.9	5	1 FARP_ARTTR	P41853 artiposthi
14	7	21.9	5	1 PAP2_PAPMA	P81864 pardachirus
15	7	21.9	5	1 PRCT_PEFAM	P01373 periplaneta
16	7	21.9	5	1 SUGA_ACHDO	P39991 acheta dome
17	7	21.9	5	1 UC22_MAIZE	P80628 zea mayis (m
18	7	21.9	6	1 ASP2_LACSN	P82655 lactobacill
19	7	21.9	6	1 CIP1_MATED	P13736 mytilus edu
20	7	21.9	6	1 CIP2_MATED	P13737 mytilus edu
21	7	21.9	6	1 EI01_LITRU	P82096 litoria rub
22	7	21.9	6	1 OVM_LEPDE	P42985 leptinotars
23	7	21.9	6	1 TMOF_SABBU	P41495 sarcophaga
24	7	21.9	6	1 TRPL_PSEPU	P36414 pseudomonas
25	7	21.9	6	1 VP19_HSVIK	P32110 herpes simp
26	6	18.8	4	1 DMS_PSECH	P19918 pseudomonas
27	6	18.8	4	1 FFKA_ATEL	P58705 anthopleura
28	5	15.6	4	1 FLRF_HIRME	P42561 hirudo medi
29	5	15.6	4	1 FLRN_ATEL	P58707 anthopleura
30	5	15.6	4	1 EMRE_MACNI	P01162 macrocallis
31	5	15.6	5	1 EI04_LITRU	P82100 litoria rub
32	5	15.6	5	1 UF01_MOUSE	P38639 mus muscullu
33	5	15.6	6	1 ACPH_RABIT	P25154 oryctolagus

34	5	15.6	6	1 FARP_MONEX	P41966 moniezia ex
35	4	12.5	3	1 LUXE_VIBFI	P24272 vibrio fisc
36	4	12.5	4	1 ACHI_ACHFU	P35904 achatina fu
37	4	12.5	5	1 BIOB_CITFR	P12997 citrobacter
38	4	12.5	5	1 RE11_LITRU	P82070 litoria rub
39	4	12.5	5	1 RE21_LITRU	P82071 litoria rub
40	4	12.5	5	1 RE31_LITRU	P82072 litoria rub
41	4	12.5	6	1 LOK1_LOCFI	P41491 locusta mig
42	3	9.4	4	1 BOS1_HUMAN	P02731 homo sapien
43	3	9.4	4	1 OCPL_OCTMI	P58648 octopus min
44	3	9.4	5	1 RE32_LITRU	P82073 litoria rub
45	3	9.4	5	1 TP12_CANFA	P54714 canis famil

ALIGNMENTS

RESULT 1
TUFT_HUMAN
ID TUFT_HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
ACTIVITY OF NEUTROPHILS.
DR PIR; A02147; A02147.
DR MIM; 191150; -.
SQ SEQUENCE 4 AA; 501 MW; 74176321C00000000 CRC64;

Query Match 37.5%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PR 2
DB 3 PR 4

RESULT 2
PSK_DAUCA
ID PSK_DAUCA STANDARD; PRT; 5 AA.
AC P58261;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta: eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
 OX NCBI_TaxID=4039;
 RN
 RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
 RC STRAIN=cv. US-Harumakigousun;
 RX MEDLINE=20212743; PubMed=10750705;
 RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
 RA Kamada H., Sakagami Y.;
 RT "A secreted peptide growth factor, phytosulfokine, acting as a
 stimulatory factor of carrot somatic embryo formation.";
 RL Plant Cell Physiol. 41:27-32(2000).
 CC -1- FUNCTION: IN PRESENCE OF 2,4-D. STIMULATES PROLIFERATION OF THE
 CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
 CC EMBRYOS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
 CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
 KW Growth factor; Sulfation.
 FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
 FT MOD_RES 1 1 SULFATION.
 FT MOD_RES 3 3 SULFATION.
 FT MOD_RES 5 5 AA; 687 MW; 76C1BB504B300000 CRC64;
 SQ SEQUENCE 5 AA; 687 MW; 76C1BB504B300000 CRC64;
 Query Match 34.4%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 IY 6
 Db 2 IY 3
 RESULT 3
 FVRL ANTEL
 ID FVRL ANTEL STANDARD; PRT; 4 AA.
 AC P59706;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Antho-Riamide I [Contains: Antho-Riamide II].
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92270459; PubMed=1821096;
 RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
 RA Grimmelikhuijzen C.J.P.;
 RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
 RT biologically active L-3-phenylactyl-Tyr-Arg-Ile-NH2 and its
 RT des-phenylactyl fragment Tyr-Arg-Ile-NH2.";
 RL Peptides 12:1165-1173(1991).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two
 RT inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
 RL Proc. R. Soc. Lond. B Biol. Sci. 253:183-188(1993).
 CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
 CC groups. May be involved in the expansion phase of feeding
 CC behaviour in sea anemones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron-specific.
 DR InterPro: IPR001023; Hsp70.
 KW Neuropeptide; Amidation.
 FT CHAIN 1 4 ANTHO-RIAMIDE I.
 FT CHAIN 2 4 ANTHO-RIAMIDE II.
 FT MOD_RES 1 1 L-3-PHENYLACTYL.
 FT MOD_RES 4 4 AMIDATION.

SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;
 Query Match 28.1%; Score 9; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 RI 5
 Db 3 RI 4
 RESULT 4
 UN06_CLOPA
 ID UN06_CLOPA STANDARD; PRT; 6 AA.
 AC P81351; 1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 6 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
 FT NON_TER 6
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 657 MW; 605B1D1CA45A8000 CRC64;
 Query Match 25.0%; Score 8; DB 1; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 ARI 5
 Db 4 AEI 6
 RESULT 5
 THYL_PIG
 ID THYL_PIG STANDARD; PRT; 3 AA.
 AC P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
 OS Sus scrofa (Pig).
 OS Ovis aries (Sheep).
 OS Bombina orientalis (Oriental fire-bellied toad), and
 OS Neophthalmus viridescens (Eastern newt) (Triturus viridescens).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823, 9940, 8346, 8316;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=PIG; TISSUE=Hypothalamus;
 RX MEDLINE=70136150; PubMed=4984938;
 RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
 RT "Structure of porcine thyrotropin releasing hormone.";
 RL Biochemistry 9:1103-1106(1970).
 RN [2]
 RP SYNTHESIS.
 RC SPECIES=PIG;
 RX MEDLINE=70039904; PubMed=4982117;
 RA Bolter J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
 RT "The identity of chemical and hormonal properties of the thyrotropin

RT releasing hormone and pyroglutamyl-histidyl-proline amide.";
 RL Blochem. Biophys. Res. Commun. 37:705-710(1969).
 RP [3]
 RC SPECIES=Sheep; TISSUE=Hypothalamus;
 RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,
 RA Ward D.N.;
 RT "The elucidation of the primary structure of the hypothalamic thyroid
 RT stimulating hormone releasing factor of ovine origin by means of mass
 RT spectrometry.";
 RL Org. Mass Spectrom. 5:221-228(1971).
 RP [4]
 RP SYNTHESIS.
 RC SPECIES=Sheep;
 RX MEDLINE=70163386; PubMed=4985794;
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
 RA Guillemin R.;
 RT "Characterization of ovine hypothalamic hypophysiotropic
 RT TSH-releasing factor.";
 RL Nature 226:321-325(1970).
 RP [5]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Skin;
 RX MEDLINE=76138399; PubMed=815011;
 RA Yasuhara T., Nakajima T.;
 RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 RP [6]
 RP SEQUENCE.
 RC SPECIES=N.Viridescens;
 RX MEDLINE=75035605; PubMed=4214528;
 RA Grimm-Joergensen Y., McKelvy J.F.;
 RT "Biosynthesis of tyrotropin releasing factor by newt (Triturus
 RT viridescens) brain in vitro. Isolation and characterization of
 RT tyrotropin releasing factor.";
 RL J. Neurochem. 23:471-478(1974).
 CC -|- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
 CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
 CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
 DR PIR; A01415; RHPGT.
 DR PIR; A93750; RHSHT.
 DR PIR; A90919; RHTDQ.
 DR PIR; A92971; A92971.
 KW Amidation.
 FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 3 3 AMIDATION.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;
 Query Match 21.9%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 P 1
 Db 3 P 3

RESULT 6
 DCML_PSECH
 ID DCML_PSECH STANDARD; PRT; 4 AA.
 AC F19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN Cudi.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxyotrophic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -|- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -|- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -|- COFACTOR: Molybdenum (molybdopterin).
 CC -|- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR; P0140; P0140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;
 Query Match 21.9%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 P 1
 Db 4 P 4

RESULT 7
 FAR3_HIRME
 ID FAR3_HIRME STANDARD; PRT; 4 AA.
 AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide YLRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arynchobellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD.RES 4 4
 FT MOD.RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
 Query Match 21.9%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 Y 6
 Db 1 Y 1

RESULT 8
 FAR4_HIRME
 ID FAR4_HIRME STANDARD; PRT; 4 AA.
 AC P42563;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide YLRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arynchobellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.

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RX MEDLINE-92195954; PubMed-1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation.
KW MOD_RES 4 4 AMIDATION.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 Y 6
DB 1 Y 1

RESULT 9
RM01_YEAST
ID RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
[1]
RN SEQUENCE.
RX MEDLINE-91285106; PubMed-2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
DR PIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1
DB 4 P 4

RESULT 10
AL14_CARMA
ID AL14_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
[1]
RN SEQUENCE.
RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE-96121193; PubMed-9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,

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RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -|- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -|- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
CC Neuropeptide; Amidation; Multigene family.
KW MOD_RES 5 5 AMIDATION (POTENTIAL).
FT MOD_RES 5 5 AMIDATION (POTENTIAL).
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 Y 6
DB 1 Y 1

RESULT 11
BPP7_BOTIN
ID BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
[1]
RN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE-90351557; PubMed-2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -|- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1
DB 5 P 5

RESULT 12
EI03_LITRU
ID EI03_LITRU STANDARD; PRT; 5 AA.
AC P82099;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
[1]
RN

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RP SEQUENCE.
RC TISSUE-Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -|- SUBCELLULAR LOCATION: SECRETED.
KW Amphibian skin; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1
Db 4 P 4

RESULT 13
FARP_ARTTR STANDARD; PRT; 5 AA.
AC PA1853;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRFamide-like neuropeptide RYIRF-amide.
OS Artiposthia triangulata.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Terricola; Geoplanidae; Arthurdendyus.
OX NCBI_TaxID=132421;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=94211927; PubMed=7909164;
RA Maule A.G., Shaw C., Hallton D.W., Curry W.J., Thim L.;
RT "RYIRFamide: a turbellarian FMRFamide-related peptide (FARP).";
RL Regul. Pept. 50:37-43(1994).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 Y 6
Db 2 Y 2

RESULT 14
PAP2_PARMA STANDARD; PRT; 5 AA.
AC PA1864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moles sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleioidi; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE-Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;

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RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moles sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -|- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC -|- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC -|- SUBCELLULAR LOCATION: Secreted.
KW Toxin.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1
Db 5 P 5

RESULT 15
PRCT_PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES-P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES-P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]
RP SEQUENCE.
RC SPECIES-L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES-C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -|- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.

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CC -I- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.

DR PIR: A01644: HOROHA.
 DR PIR: A60411: A60411.

KW Neuropeptide.

SQ SEQUENCE 5 AA; 649 MW; 71B7673B4600000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Y 6

Db 2 Y 2

Search completed: December 12, 2002, 15:19:17

Job time : 8.2 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:09:54 ; Search time 25.5 Seconds
(without alignments)
48.482 Million cell updates/sec

Title: US-09-600-432-24
Perfect score: 32
Sequence: 1 PRARIY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPTEMBL21.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	21.9	5	13 P83308	P83308 gallus gall
2	7	21.9	6	10 P82181	P82181 spinacia ol
3	7	21.9	6	10 P82182	P82182 spinacia ol
4	6	18.8	6	10 P82541	P82541 spinacia ol
5	4	12.5	5	10 Q99007	Q99007 hordeum vul
6	3	9.4	4	11 Q08433	Q08433 rattus norv
7	2	6.2	5	2 P83073	P83073 bacillus ce

ALIGNMENTS

RESULT 1
P83308
ID P83308
AC P83308; PRELIMINARY; PRT; 5 AA.

DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE FMRFamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=BRAIN.
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.; "A novel active pentapeptide from chicken brain identified by antibodies to FMRFamide.";
RL Nature 305:328-330(1983).
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;
Query Match 21.9%; Score 7; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 P 1
Db 2 P 2
RESULT 2
P82181
ID P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
DT 01-JUN-2000 (TEMBLrel. 14, Created)
DT 01-JUN-2000 (TEMBLrel. 14, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OC NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.; "The plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR001790; Ribosomal L10.
DR InterPro: IPR002363; Ribosomal L10eub.
DR Pfam: PF00466; Ribosomal L10; PARTIAL.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB0000 CRC64;
Query Match 33.3%; Score 7; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 RAR 4
Db 4 RTK 6

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RESULT 3
P82182 ID P82182 PRELIMINARY; PRT; 6 AA.
AC P82182;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001790; Ribosomal_L10.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 675 MW; 63218415B05DB000 CRC64;

Query Match 21.9%; Score 7; DB 10; Length 6;
Best Local Similarity 33.3%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RA 4
I:
DB 4 RTK 6

RESULT 4
P82541 ID P82541 PRELIMINARY; PRT; 6 AA.
AC P82541;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435797; PubMed=10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28455-28465(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -1- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA

FORM IS THE MINOR BASIC FORM.
-1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
-1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; PARTIAL.
DR PRINTS; PR00975; RIBOSOMALS19; PARTIAL.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 18.8%; Score 6; DB 10; Length 6;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RA 3
I:
DB 2 RS 3

RESULT 5
Q99007 ID Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1) (Fragment).
GN AMYL.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic
acid and abscisic acid in protoplasts prepared from mature barley
aleurone layers.";
RL Plant Mol. Biol. 16:713-721(1991).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
BARLEY.
DR EMBL; X54643; CAA38455.1; -.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON_TER 5
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 12.5%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 A 3
I:
DB 2 A 2

RESULT 6
Q08433 ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT
(Fragment)).
OS Rattus norvegicus (Rat).
```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GUNN;
 RX MEDLINE=91282758; PubMed=1840486;
 RA Sato H., Aono S., Kaishimata S., Koizumi O.;
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 RT hyperbilirubinemic Gunn rat.";
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS.
 CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 CC -!- SUBCELLULAR LOCATION: MICROSOME.
 CC EMBL; S38636; AA019259.1; -.
 DR Transferase; Glycosyltransferase; Microsome; Multigene family.
 KW NON_TER 1 1
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 9.4%; Score 3; DB 11; Length 4;
 Best Local Similarity 0.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 I 5
 ;
 Db 2 V 2

RESULT 7

P83073
 ID P83073 PRELIMINARY; PRT; 5 AA.
 AC P83073;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE 88 kDa protein (Fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 6.2%; Score 2; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
 ;
 Db 2 K 2

Search completed: December 12, 2002, 15:18:46
 Job time : 25.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:09:28 ; Search time 27 Seconds
(without alignments)
24.676 Million cell updates/sec

Title: US-09-600-432-25

Perfect score: 25

Sequence: 1 RARY 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 42205

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
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- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	5	20	AA198512
2	25	100.0	5	21	AA19067
3	25	100.0	6	20	AA198511
4	25	100.0	6	21	AA19065
5	20	80.0	4	20	AA198513
6	20	80.0	4	21	AA19068
7	19	76.0	6	20	AA198542
8	18	72.0	5	18	AA19842
9	18	72.0	5	20	AA198546
10	18	72.0	5	21	AA19066

11	18	72.0	5	22	AA11144	Chymotryptic pepti
12	17	68.0	6	17	AAW08720	Trypsin inhibitory
13	17	68.0	6	17	AAW08721	Trypsin inhibitory
14	17	68.0	6	17	AAW08722	Trypsin inhibitory
15	17	68.0	6	17	AAW0652	S. acidocaldarius
16	17	68.0	6	18	AA15886	Peptide derivative
17	17	68.0	6	19	AAW0768	Heparin sulfate bi
18	17	68.0	6	19	AAW5694	Enzyme inhibitor p
19	17	68.0	6	20	AA122420	Fibronectin peptid
20	17	68.0	6	21	AA101581	Proteoglycan bindi
21	17	68.0	6	23	AAW85707	Extra cellular mat
22	17	68.0	6	23	AAU11029	Recombinant RSV ge
23	16	64.0	4	10	AA191620	Motif useful in to
24	16	64.0	4	19	AAW5761	Immunisation motif
25	16	64.0	4	22	AAW86383	Cathepsin derived
26	16	64.0	5	5	AA10816	Sequence of fragme
27	16	64.0	5	7	AA10156	Human growth hormo
28	16	64.0	5	16	AAW69079	C-terminal of Grow
29	16	64.0	5	20	AA128184	Factor Xa inhibiti
30	16	64.0	5	21	AAW06421	Claudin-1 cell adh
31	16	64.0	6	21	AAW06422	Claudin-1 cell adh
32	16	64.0	6	21	AAW06424	Claudin-1 cell adh
33	16	64.0	6	21	AAW06510	Claudin-1 cyclic c
34	16	64.0	6	21	AAW69272	Peptide which inhi
35	16	64.0	6	23	AAU93629	Granulocyte-colony
36	15	60.0	3	15	AAW61094	ACE-inhibiting tri
37	15	60.0	4	17	AAW95671	Angiotensin II fra
38	15	60.0	4	19	AAW64737	Angiotensin II pep
39	15	60.0	4	19	AAW65606	Angiotensin II ana
40	15	60.0	4	19	AAW71119	Peptide AII(1-4) u
41	15	60.0	4	20	AA149595	Angiotensin analog
42	15	60.0	4	20	AA133910	Angiotensin II ana
43	15	60.0	4	20	AA130548	Amino acid sequenc
44	15	60.0	4	20	AA130592	Amino acid sequenc
45	15	60.0	4	20	AA132723	Angiotensin II ana

ALIGNMENTS

RESULT 1
AA128512
ID AA128512 standard; peptide; 5 AA.
AC AA128512;
XX:
DT 19-OCT-1999 (first entry)
XX:
DE Beta-1 integrin cell adhesion modulator analogue #25.
XX:
KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
OS Synthetic.
PN WO9937669-A1.
XX:
PD 29-JUL-1999.
XX:
PF 21-JAN-1999; 99WO-US01236.
XX:
PR 12-AUG-1998; 98US-0096212.
PR 22-JAN-1998; 98US-0072119.
PR 12-AUG-1998; 98US-0096211.
(MINU) UNIV MINNESOTA.
PI Brienza A, Furcht LT, McCarthy JB;
DR WPI; 1999-469112/39.
XX:
PT New peptides modulating beta1 integrin subunit dependent cell
adhesion, useful to study cell adhesion e.g. alpha4beta1 integrin

PT dependent adhesion important in tumour cell biology
 PS Claim 6; Fig 7; 47pp; English.
 XX This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAY28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which
 CC has a side chain including an aromatic group, and a penultimate
 CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
 CC a 'lipar' motif. Studies with these peptides have also shown that
 CC inhibiting peptides do not contain D-amino acids and that it is the
 CC presence of the ArLip motif that conveys effective beta1 integrin
 CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
 CC cell adhesion is important for cell adhesion to extracellular matrix
 CC proteins, and the subunit is expressed on tumours such as melanomas.
 CC Therefore these Lipar motif containing peptides may be important in the
 CC treatment of cancer.
 XX SQ Sequence 5 AA;
 Query Match 100.0%; Score 25; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RARIY 5
 Db 1 RARIY 5
 RESULT 2
 AAB19067
 ID AAB19067 standard; peptide; 5 AA.
 AC AAB19067;
 XX 08-FEB-2001 (first entry)
 DT Amino acid sequence of a beta1-integrin inhibitor.
 DE Beta1-integrin inhibitor; leukocyte mediated tissue destruction;
 KW central nervous system ischemic injury; myocardial infarction;
 KW beta1-integrin; angioplasty; surgical incision; injury-related trauma;
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX Synthetic.
 OS WO200056350-A2.
 PN 28-SEP-2000.
 XX 22-MAR-2000; 2000WO-US07680.
 PF 22-MAR-1999; 99US-0125634.
 PR 24-NOV-1999; 99US-0167538.
 XX (MINU) UNIV MINNESOTA.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (SENT-) SENTRON MEDICAL INC.
 XX McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
 PI Furcht LT;
 PI WPI; 2000-656062/63.
 DR Inhibition of inflammatory leukocyte mediated destruction of tissue in
 XX a patient, comprises administering a peptide inhibitor of
 PT beta1-integrin, useful for treatment of e.g. cancer and osteoporosis -
 PT Claim 3; Page 38; 61pp; English.
 PS AAB19054-67 represent beta1-integrin inhibitors. The peptides inhibit
 XX beta1-integrin which is responsible for leukocyte mediated tissue

CC destruction. The peptides are useful for inhibiting inflammatory
 CC leukocyte mediated destruction of tissue which occurs as a result of
 CC central nervous system (CNS) ischemic injury, myocardial infarction,
 CC angioplasty, surgical incisions, injury-related trauma, and/or
 CC transplant reperfusion, exposure to heat, cold, light, electricity
 CC and/or chemicals. They are also useful for the treatment of stroke, a
 CC burn type injury, cancer, and osteoporosis.
 XX SQ Sequence 5 AA;
 Query Match 100.0%; Score 25; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RARIY 5
 Db 1 RARIY 5
 RESULT 3
 AAY28511
 ID AAY28511 standard; peptide; 6 AA.
 XX AC AAY28511;
 XX 19-OCT-1999 (first entry)
 DT Beta-1 integrin cell adhesion modulator analogue #24.
 DE Beta 1 integrin dependent cell adhesion; Lipar motif; tumour;
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX Synthetic.
 OS WO9937669-A1.
 PN 29-JUL-1999.
 XX 21-JAN-1999; 99WO-US01236.
 PF 12-AUG-1998; 98US-0096212.
 PR 22-JAN-1998; 98US-0072119.
 PR 12-AUG-1998; 98US-0096211.
 XX (MINU) UNIV MINNESOTA.
 PA Brienzo A, Furcht LT, McCarthy JB;
 PI WPI; 1999-469112/39.
 DR New peptides modulating beta1 integrin subunit dependent cell
 PT adhesion, useful to study cell adhesion e.g. alpha4beta1 integrin
 PT dependent adhesion important in tumour cell biology
 XX Claim 6; Fig 7; 47pp; English.
 XX This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAY28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which
 CC has a side chain including an aromatic group, and a penultimate
 CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
 CC a 'lipar' motif. Studies with these peptides have also shown that
 CC inhibiting peptides do not contain D-amino acids and that it is the
 CC presence of the ArLip motif that conveys effective beta1 integrin
 CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
 CC cell adhesion is important for cell adhesion to extracellular matrix
 CC proteins, and the subunit is expressed on tumours such as melanomas.
 CC Therefore these Lipar motif containing peptides may be important in the
 CC treatment of cancer.
 XX SQ Sequence 6 AA;

Query Match 100.0%; Score 25; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RARIY 5
 Db 2 RARIY 6
 |||||

RESULT 4
 AAB19065
 ID AAB19065 standard; peptide; 6 AA.
 AC AAB19065;
 XX
 XX 08-FEB-2001 (first entry)
 DT
 XX
 DE Amino acid sequence of a betal-integrin inhibitor.
 XX
 KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
 KW central nervous system ischemic injury; myocardial infarction;
 KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX
 OS Synthetic.
 XX
 PN W0200056350-A2.
 XX
 XX 28-SEP-2000.
 XX
 XX 22-MAR-2000; 2000WO-US07680.
 XX
 PR 22-MAR-1999; 99US-0125634.
 PR 24-NOV-1999; 99US-0167538.
 XX
 XX (MINU) UNIV MINNESOTA.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (SENT -) SENTRON MEDICAL INC.
 XX
 PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
 PI Furcht LT;
 PI WPI; 2000-656062/63.
 DR
 XX Inhibition of inflammatory leukocyte mediated destruction of tissue in
 PT a patient, comprises administering a peptide inhibitor of
 PT betal-integrin, useful for treatment of e.g. cancer and osteoporosis -
 XX
 PS Claim 3; Page 38; 61pp; English.
 XX
 CC AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
 CC betal-integrin which is responsible for leukocyte mediated tissue
 CC destruction. The peptides are useful for inhibiting inflammatory
 CC leukocyte mediated destruction of tissue which occurs as a result of
 CC central nervous system (CNS) ischemic injury, myocardial infarction,
 CC angioplasty, surgical incisions, injury-related trauma, and/or
 CC transplant reperfusion, exposure to heat, cold, light, electricity
 CC and/or chemicals. They are also useful for the treatment of stroke, a
 CC burn type injury, cancer, and osteoporosis.
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 25; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RARIY 5
 Db 2 RARIY 6
 |||||

RESULT 5
 AAY28513

ID AAY28513 standard; peptide; 4 AA.
 XX
 AC AAY28513;
 XX
 DT 19-OCT-1999 (first entry)
 XX
 DE Beta-1 integrin cell adhesion modulator analogue #26.
 XX
 KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX
 OS Synthetic.
 XX
 PN W09937669-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 21-JAN-1999; 99WO-US01236.
 XX
 PR 12-AUG-1998; 98US-0096212.
 PR 22-JAN-1998; 98US-0072119.
 PR 12-AUG-1998; 98US-0096211.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Brienza A, Furcht LT, McCarthy JB;
 XX
 DR WPI; 1999-469112/39.
 XX
 PT New peptides modulating betal integrin subunit dependent cell
 PT adhesion, useful to study cell adhesion e.g. alpha4betal integrin
 PT dependent adhesion important in tumour cell biology
 XX
 PS Claim 6; Fig 8; 47pp; English.
 XX
 CC This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAY28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which
 CC has a side chain including an aromatic group, and a penultimate
 CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
 CC a 'LipAr' motif. Studies with these peptides have also shown that
 CC inhibiting peptides do not contain D-amino acids and that it is the
 CC presence of the ArLip motif that conveys effective betal integrin
 CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
 CC cell adhesion is important for cell adhesion to extracellular matrix
 CC proteins, and the subunit is expressed on tumours such as melanomas.
 CC Therefore these LipAr motif containing peptides may be important in the
 CC treatment of cancer.
 XX
 SQ Sequence 4 AA;

Query Match 80.0%; Score 20; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RARIY 5
 Db 1 RARIY 4
 |||||

RESULT 6
 AAB19068
 ID AAB19068 standard; peptide; 4 AA.
 XX
 AC AAB19068;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of a betal-integrin inhibitor.
 XX
 KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
 KW central nervous system ischemic injury; myocardial infarction;

KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX Synthetic.
 XX WO200056350-A2.
 XX 28-SEP-2000.
 XX 22-MAR-2000; 2000WO-US07680.
 XX 22-MAR-1999; 99US-0125634.
 XX 24-NOV-1999; 99US-0167538.
 XX (MINU) UNIV MINNESOTA.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX (SENT-) SENTRON MEDICAL INC.
 XX McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
 PI Furcht LF;
 XX WPI: 2000-656062/63.
 XX Inhibition of inflammatory leukocyte mediated destruction of tissue in
 PT a patient, comprises administering a peptide inhibitor of
 PT betal-integrin, useful for treatment of e.g. cancer and osteoporosis -
 XX
 PS Claim 3; Page 38; 61pp; English.
 XX AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
 CC betal-integrin which is responsible for leukocyte mediated tissue
 CC destruction. The peptides are useful for inhibiting inflammatory
 CC leukocyte mediated destruction of tissue which occurs as a result of
 CC central nervous system (CNS) ischemic injury, myocardial infarction,
 CC angioplasty, surgical incisions, injury-related trauma, and/or
 CC transplant reperfusion, exposure to heat, cold, light, electricity
 CC and/or chemicals. They are also useful for the treatment of stroke, a
 CC burn type injury, cancer, and osteoporosis.
 XX
 SQ Sequence 4 AA;
 Query Match 80.0%; Score 20; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ARIY 5
 DB 1 ARIY 4
 RESULT 7
 ID AAY25842 standard; Protein; 6 AA.
 XX
 AC AAY25842;
 XX
 DT 04-OCT-1999 (first entry)
 XX
 DE Human secreted protein fragment encoded from gene 49.
 XX
 KW Secreted protein; human; treatment; diagnosis; therapy; cancer; tumour;
 KW neurodegenerative disorder; developmental abnormality; blood disorder;
 KW fetal deficiency; blood disorder; leukemia; immune system; inflammation;
 KW autoimmune disease; hepatic disease; renal disease; allergy; restenosis;
 KW ischaemic shock; Alzheimer's disease; cognitive disorder; schizophrenia;
 KW cardiovascular disorder; wound healing; stroke; arthritis; obesity;
 KW asthma; sepsis; acne; psoriasis; transplant rejection; infection; AIDS;
 KW metabolic disorder.
 XX Homo sapiens.
 OS
 XX WO9938881-A1.
 PN
 XX

PD 05-AUG-1999.
 XX
 PF 27-JAN-1999; 99WO-US01621.
 XX
 PR 30-JAN-1998; 98US-0073170.
 PR 30-JAN-1998; 98US-0073159.
 PR 30-JAN-1998; 98US-0073160.
 PR 30-JAN-1998; 98US-0073161.
 PR 30-JAN-1998; 98US-0073162.
 PR 30-JAN-1998; 98US-0073164.
 PR 30-JAN-1998; 98US-0073165.
 PR 30-JAN-1998; 98US-0073167.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Carter KC, Endress GA, Feng P, Ferrie AM, Florence C;
 PI Florence KA, Janat F, Ni J, Rosen CA, Ruben SM;
 PI Soppet DR, Young P, Yu G;
 XX
 XX WPI: 1999-469315/39.
 DR N-PSDB; AAZ00458.
 DR
 XX New isolated human genes and the secreted polypeptides they encode
 PT useful in, e.g. treatment of Alzheimer's
 PT
 XX Disclosure; Page 365; 393pp; English.
 XX
 CC This invention describes novel human genes (see AAZ00410-Z00477) and the
 CC secreted proteins (see AAY25711-Y25778) and fragments (see
 CC AAY25779-Y25907) they encode. The polynucleotides and their corresponding
 CC secreted polypeptides are useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. Also pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 67
 CC polynucleotides of the invention, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis
 CC or treatment of cancer, tumours, neurodegenerative disorders,
 CC developmental abnormalities and fetal deficiencies, blood disorders,
 CC leukemias, diseases of the immune system, autoimmune diseases, hepatic
 CC and renal disease, inflammation, allergies, ischaemic shock, Alzheimer's
 CC and cognitive disorders, schizophrenia, restenosis, cardiovascular
 CC disorders, wound healing, stroke, arthritis, obesity, asthma, sepsis,
 CC acne, psoriasis, transplant rejection, metabolic disorders, infections
 CC and AIDS. The polypeptides are also useful for identifying their binding
 CC partners.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 76.0%; Score 19; DB 20; Length 6;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ARIY 5
 DB 1 ARIY 4
 RESULT 8
 ID AAW19842
 ID AAW19842 standard; Peptide; 5 AA.
 XX
 AC AAW19842;
 XX
 DT 26-JAN-1998 (first entry)
 XX
 DE Chimeric adenovirus coat protein heparin binding motif.
 XX Adenovirus; vector; coat protein; gene therapy; gene transfer;
 KW human; cancer; autoimmune disease; heart disease; infection;
 KW heparin.
 XX
 OS Synthetic.

```

XX PN W09720051-A2.
XX PD 05-JUN-1997.
XX PF 27-NOV-1996; 96WO-US19150.
XX PR 21-AUG-1996; 96US-0701124.
XX PR 28-NOV-1995; 95US-0563368.
XX PR 21-AUG-1996; 96US-0700846.
XX PA (GENV-) GENVEC INC.
XX PI Brough DE, Kovessi I, Wickham TJ;
XX DR WPI; 1997-310606/28.
XX PT Adenoviral vectors containing chimeric coat protein - bind and enter
XX PT cells more efficiently, useful for gene therapy of e.g. cancer,
XX PT autoimmune diseases, etc.
XX PS Claim 7; Page 19; 121pp; English.
XX CC This peptide is used as a universal transfer vector (UTV) sequence
XX CC or as a spacer sequence in novel chimeric adenovirus coat proteins
XX CC (CP), especially chimeric fibre proteins. It comprises a heparin
XX CC binding motif derived from fibronectin. Claimed UTVs/spacers are
XX CC given in AAW19810-11, AAW19813-25, AAW19827, AAW19829, AAW19831-32 and
XX CC AAW19834-43). Claimed chimeric CPs differ from the wild-type CP by the
XX CC introduction of the UTV and/or spacer at or near the C-terminus or
XX CC in an exposed loop. This imparts on the chimeric CP the ability to
XX CC bind to and enter cells by means of a novel cell surface binding
XX CC site. Recombinant vectors comprising the chimeric CP are able to
XX CC enter cells more efficiently than vectors comprising wild-type CP,
XX CC especially at lower m.o.i. They are especially useful for gene
XX CC therapy of e.g. cancers, genetic disorders, pathogenic infections,
XX CC heart disease or autoimmune diseases.
XX SQ Sequence 5 AA;
Query Match 72.0%; Score 18; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RARI 4
Db 1111
2 RARI 5
RESULT 9
AAI28546
ID AAY28546 standard; peptide; 5 AA.
XX AC AAY28546;
XX DT 19-OCT-1999 (first entry)
XX DE Beta-1 integrin cell adhesion modulator analogue #39.
XX KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
XX KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
XX OS Synthetic.
XX PN W09937669-A1.
XX PD 29-JUL-1999.
XX PF 21-JAN-1999; 99WO-US01236.
XX PR 12-AUG-1998; 98US-0096212.
XX PR 22-JAN-1998; 98US-0072119.
XX PR 12-AUG-1998; 98US-0096211.

```

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XX PA (MINU ) UNIV MINNESOTA.
XX PI Brienza A, Furcht LT, McCarthy JB;
XX DR WPI; 1999-469112/39.
XX PT New peptides modulating betal integrin subunit dependent cell
XX PT adhesion, useful to study cell adhesion e.g. alphadbetal integrin
XX PT dependent adhesion important in tumour cell biology
XX PS Example 11; Fig 15; 47pp; English.
XX CC This peptide is used with AAY28510-Y28549 to show that peptides
XX CC which modulate beta-1 integrin subunit dependent cell adhesion need a
XX CC C-terminal amino acid residue (Ar) which has a side chain including an
XX CC aromatic group. They also need a penultimate C-terminal amino acid
XX CC residue (Lip) with an alkyl side chain group, i.e. a 'LipAr' motif.
XX CC Studies with these peptides have also shown that inhibiting peptides do
XX CC not contain D-amino acids and that it is the presence of the ArLip motif
XX CC that conveys effective betal integrin dependent cell adhesion is
XX CC inhibition. The beta-1 integrin subunit dependent cell adhesion is
XX CC important for cell adhesion to extracellular matrix proteins, and the
XX CC subunit is expressed on tumours such as melanomas. Therefore these LipAr
XX CC motif containing peptides may be important in the treatment of cancer.
XX SQ Sequence 5 AA;
Query Match 72.0%; Score 18; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RARI 4
Db 1111
2 RARI 5
RESULT 10
AAB19066
ID AAB19066 standard; peptide; 5 AA.
XX AC AAB19066;
XX DT 08-FEB-2001 (first entry)
XX DE Amino acid sequence of a betal-integrin inhibitor.
XX KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
XX KW central nervous system ischemic injury; myocardial infarction;
XX KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
XX KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
XX OS Synthetic.
XX PN W0200056350-A2.
XX PD 28-SEP-2000.
XX PF 22-MAR-2000; 2000WO-US07680.
XX PR 22-MAR-1999; 99US-0125634.
XX PR 24-NOV-1999; 99US-0167538.
XX PA (MINU ) UNIV MINNESOTA.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PA (SENT-) SENTRON MEDICAL INC.
XX PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
XX PI Furcht LT;
XX DR WPI; 2000-656062/63.
XX PT Inhibition of inflammatory leukocyte mediated destruction of tissue in

```

PT a patient, comprises administering a peptide inhibitor of
PT betal-integrin, useful for treatment of e.g. cancer and osteoporosis
XX
PS Claim 3; Page 38; 6lpp; English.
XX
CC AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
CC betal-integrin which is responsible for leukocyte mediated tissue
CC destruction. The peptides are useful for inhibiting inflammatory
CC leukocyte mediated destruction of tissue which occurs as a result of
CC central nervous system (CNS) ischemic injury, myocardial infarction,
CC angiolplasty, surgical incisions, injury-related trauma, and/or
CC transplant reperfusion, exposure to heat, cold, light, electricity
CC and/or chemicals. They are also useful for the treatment of stroke, a
CC burn type injury, cancer, and osteoporosis.
XX
SQ Sequence 5 AA;
Query Match 72.0%; Score 18; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RARI 4
| | | |
Db 2 RARI 5

RESULT 11
AAE11144
ID AAE11144 standard; peptide; 5 AA.
XX
AC AAE11144;
XX
DT 18-DEC-2001 (first entry)
XX
DE Chymotryptic peptide #14 of phhAB fusion protein.
XX
KW Phenylalanine hydroxylase; PAH; phhA: 4a-carbinolamine dehydratase; phhB;
KW aromatic aminotransferase; phhC; milk protein; animal protein; casein;
KW proteinaceous food product; globulin; whey protein; phenylketonuria;
KW PKU; inherited metabolic disorder; impaired brain function; nootropic;
KW cell therapy; chymotryptic peptide.
XX
OS Unidentified.
XX
XX WO200168822-A2.
PN
XX 20-SEP-2001.
PD
XX
PF 14-MAR-2001; 2001WO-DK00172.
XX
PR 14-MAR-2000; 2000US-0525116.
XX
XX (NILA-) NILAB APS.
XX
XX Johnsen M, Ravn P, Madsen SM, Vrang A, Israelsen H, Bredmose L;
PI Arnau J, Jensen SH, Gjetting T, Nielsen E;
XX
XX WPI; 2001-590055/66.
XX
XX Novel recombinant cells comprising a nucleic acid encoding a gene
PT product having phenylalanine hydroxylase activity, that is derived from
PT a prokaryotic organism, is useful for treating phenylketonuria in
PT mammals -
XX
XX Example 8; Page 48; 9lpp; English.
XX
CC The patent discloses novel cells comprising a nucleic acid encoding
CC a gene product having phenylalanine hydroxylase (PAH) activity such
CC as phenylalanine hydroxylase (phhA), 4a-carbinolamine dehydratase
CC (phhB) and aromatic aminotransferase (phhC), which are derived
CC from a prokaryotic organism. The patent also relates to fusion
CC proteins comprising a protein enhancing and/or stabilising the
CC PAH activity in addition to PAH activity. The cells are useful

CC for producing PAH. The sequences of the invention are also useful
CC for preparing a proteinaceous food product (animal protein such
CC as a milk protein derived from casein, globulin or a whey protein)
CC having reduced content of phenylalanine. The method involves contacting
CC the food product starting material with the cells or fusion proteins
CC such that at least part of the phenylalanine content of the starting
CC material is converted into compounds that do not cause phenylketonuria
CC (PKU) by the enzymatically active product. PAH enzyme is useful for
CC manufacturing a medicament for treating PKU, which is an inherited
CC metabolic disorder resulting in an accumulation in the body of
CC L-phenylalanine and metabolites that can cause impaired brain
CC function. The present sequence is chymotryptic peptide of phhAB fusion
CC protein.
XX
SQ Sequence 5 AA;
Query Match 72.0%; Score 18; DB 22; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 ARY 5
| | | |
Db 2 ARY 5

RESULT 12
AAW08720
ID AAW08720 standard; peptide; 6 AA.
XX
AC AAW08720;
XX
DT 28-FEB-1997 (first entry)
XX
DE Trypsin inhibitory peptide #1.
XX
KW Ligand; synthetic combinatorial peptide library; hexamer; antibody;
KW antigen; receptor; inhibitor; trypsin.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /label= OTHER
FT /note= "Ac-Ala"
FT Modified-site 6
FT /label= OTHER
FT /note= "Pro-NH2"
XX
XX US5556762-A.
XX
XX 17-SEP-1996.
XX
XX 21-NOV-1990; 90US-0617023.
XX
XX 11-SEP-1992; 92US-0943709.
XX 21-NOV-1990; 90US-0617023.
XX 16-MAY-1991; 91US-0701658.
XX 19-NOV-1991; 91US-0797551.
XX
XX (HOUG-) HOUGHTEN PHARM INC.
XX Appel JR, Houghten RA, Pinilla C;
XX WPI; 1996-432985/43.
XX
XX Identifying oligopeptide ligands for an acceptor - by scanning
PT synthetic peptide combinatorial libraries comprising
PT self-solubilising, unsupported mixed oligopeptide(s)
XX
XX Example 8; Column 59; 75pp; English.
XX
XX The invention relates to a method of identifying oligopeptide ligands to
CC a protein by scanning synthetic combinatorial peptide libraries (SCPL).

CC The SCPL comprise sets of hexamers which contain either one of 6
 CC predetermined amino acids at one predetermined position in the hexamer
 CC and each set may have one predetermined amino acid at 1 of 6
 CC predetermined pos. in the hexamer. The method is useful for identifying
 CC biologically active sequences of e.g. pharmaceutical use. The peptides
 CC esp. inhibit the binding of e.g. an antibody to its antigen, a ligand to
 CC its receptor, etc.
 CC The peptides AAW08720-25 are N-terminally acylated and C-terminally
 CC amidated peptides, isolated from a SCPL, which inhibit trypsin.
 CC This peptide inhibited trypsin with an IC50 of 46 micromole.

XX
 SQ Sequence 6 AA;
 Query Match 68.0%; Score 17; DB 17; Length 6;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ARIY 5
 DB 1 AKIY 4

RESULT 13

AAW08721
 ID AAW08721 standard; peptide; 6 AA.

AC AAW08721;

XX 28-FEB-1997 (first entry)

XX Trypsin inhibitory peptide #2.

XX Ligand; synthetic combinatorial peptide library; hexamer; antibody;
 KW antigen; receptor; inhibitor; trypsin.

XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1
 FT /label= OTHER
 FT /note= "Ac-Ala"
 FT Modified-site 6
 FT /label= OTHER
 FT /note= "Glu-NH2"

XX US5556762-A.

XX 17-SEP-1996.

XX 21-NOV-1990; 90US-0617023.

XX 11-SEP-1992; 92US-0943709.

XX 21-NOV-1990; 90US-0617023.

XX 16-MAY-1991; 91US-0701658.

XX 19-NOV-1991; 91US-0797551.

XX (HOUG-) HOUGHTEN PHARM INC.

XX Appel JR, Houghten RA, Pinilla C;

XX WPI; 1996-432985/43.

XX Identifying oligopeptide ligands for an acceptor - by scanning

XX synthetic peptide combinatorial libraries comprising

XX self-solubilising, unsupported mixed oligopeptide(s)

XX Example 8; Column 59; 75pp; English.

XX The invention relates to a method of identifying oligopeptide ligands to

XX a protein by scanning synthetic combinatorial peptide libraries (SCPL).

XX The SCPL comprise sets of hexamers which contain either one of 6

XX predetermined amino acids at one predetermined position in the hexamer

XX and each set may have one predetermined amino acid at 1 of 6

CC predetermined pos. in the hexamer. The method is useful for identifying
 CC biologically active sequences of e.g. pharmaceutical use. The peptides
 CC esp. inhibit the binding of e.g. an antibody to its antigen, a ligand to
 CC its receptor, etc.
 CC The peptides AAW08720-25 are N-terminally acylated and C-terminally
 CC amidated peptides, isolated from a SCPL, which inhibit trypsin.
 CC This peptide inhibited trypsin with an IC50 of 108 micromole.

XX Sequence 6 AA;

Query Match 68.0%; Score 17; DB 17; Length 6;

Best Local Similarity 75.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ARIY 5

DB 1 AKIY 4

RESULT 14

AAW08722
 ID AAW08722 standard; peptide; 6 AA.

AC AAW08722;

XX 28-FEB-1997 (first entry)

XX Trypsin inhibitory peptide #3.

XX Ligand; synthetic combinatorial peptide library; hexamer; antibody;
 KW antigen; receptor; inhibitor; trypsin.

XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1
 FT /label= OTHER
 FT /note= "Ac-Ala"
 FT Modified-site 6
 FT /label= OTHER
 FT /note= "Asp-NH2"

XX US5556762-A.

XX 17-SEP-1996.

XX 21-NOV-1990; 90US-0617023.

XX 11-SEP-1992; 92US-0943709.

XX 21-NOV-1990; 90US-0617023.

XX 16-MAY-1991; 91US-0701658.

XX 19-NOV-1991; 91US-0797551.

XX (HOUG-) HOUGHTEN PHARM INC.

XX Appel JR, Houghten RA, Pinilla C;

XX WPI; 1996-432985/43.

XX Identifying oligopeptide ligands for an acceptor - by scanning

XX synthetic peptide combinatorial libraries comprising

XX self-solubilising, unsupported mixed oligopeptide(s)

XX Example 8; Column 59; 75pp; English.

XX The invention relates to a method of identifying oligopeptide ligands to

XX a protein by scanning synthetic combinatorial peptide libraries (SCPL).

XX The SCPL comprise sets of hexamers which contain either one of 6

XX predetermined amino acids at one predetermined position in the hexamer

XX and each set may have one predetermined amino acid at 1 of 6

XX predetermined pos. in the hexamer. The method is useful for identifying

XX biologically active sequences of e.g. pharmaceutical use. The peptides

XX esp. inhibit the binding of e.g. an antibody to its antigen, a ligand to

CC its receptor, etc.
CC The peptides AAW08720-25 are N-terminally acylated and C-terminally
CC amidated peptides, isolated from a SCPL, which inhibit trypsin.
CC This peptide inhibited trypsin with an IC50 of 122 micromole.
XX
XX
SQ Sequence 6 AA;

Query Match 68.0%; Score 17; DB 17; Length 6;
Best Local Similarity 75.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ARYI 5
:|:|
Db 1 AKIY 4

RESULT 15
AAR90652
ID AAR90652 standard; Peptide; 6 AA.
XX
AC AAR90652;
XX
DT 13-JUL-1996 (first entry)
XX
DE S. acidocaldarius transferase peptide fragment DN-1.
XX
KW transferase; amylase; Sulfolobus; production; alpha, alpha-trehalose;
KW malto-oligosaccharide; hydrolysis; Achromobacter; protease; digestion.
XX
OS Sulfolobus acidocaldarius.
XX
PN W09534642-A.
XX
PD 21-DEC-1995.
XX
PF 14-JUN-1995; 95WO-JP01189.
XX
PR 21-APR-1995; 95JP-0120673.
PR 15-JUN-1994; 94JP-0133354.
PR 18-AUG-1994; 94JP-0194223.
PR 31-OCT-1994; 94JP-0290394.
PR 21-NOV-1994; 94JP-0286917.
PR 21-NOV-1994; 94JP-0311185.
XX
PA (KIRI) KIRIN BEER KK.
XX
DR WPI; 1996-049671/05.
XX
PT Sulfolobus spp. derived transferase and amylase - for production of
PT alpha, alpha-trehalose from malto-oligosaccharide(s)
XX
PS Example I-11; Page 179; 357pp; Japanese.
XX
CC AAR90652-54 are Asp-N peptide fragments of a transferase isolated from
CC Sulfolobus acidocaldarius. The transferase (AAR90618) acts on a
CC saccharide having at least three sugar units, in which at least three
CC glucose units at the reducing end are alpha-1,4 linked, to transform the
CC alpha-1,4 linkages to alpha-1, alpha-1 linkages. The transferase has a
CC mol. wt. of 74 to 76 kDa. It is characterised by working at pH 4.5-6.0
CC and at 60-80 deg.C. It has an isoelectric point of 5.3-6.3 and retains
CC at least 90 percent activity after 6 hrs. at 80 deg.C. It is completely
CC inhibited by 5 mM copper sulphate. Use of the transferase and an amylase
CC in succession on suitable substrates such as malto-oligosaccharides, is
CC useful for the production of alpha, alpha-trehalose.
XX
SQ Sequence 6 AA;

Query Match 68.0%; Score 17; DB 17; Length 6;
Best Local Similarity 75.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ARYI 5
:|:|
:|:|
. . . .

Db 3 SRIY 6

Search completed: December 12, 2002, 15:17:15
Job time : 27 secs

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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:15:23 ; Search time 9.5 Seconds
(without alignments)
15.486 Million cell updates/sec

Title: US-09-600-432-25
Perfect score: 25
Sequence: 1 RARIY 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 32749

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	72.0	4	2	US-08-480-133A-15
2	18	72.0	4	3	US-09-008-308-30
3	18	72.0	5	4	US-09-101-751A-57
4	17	68.0	5	3	US-09-125-517A-42
5	17	68.0	5	4	US-09-284-625-6
6	17	68.0	6	2	US-08-616-669A-57
7	17	68.0	6	3	US-09-125-517A-8
8	17	68.0	6	4	US-09-326-440-57
9	17	68.0	6	4	US-09-057-052-7
10	16	64.0	4	3	US-09-008-308-29
11	16	64.0	5	1	US-08-095-162-22
12	16	64.0	5	1	US-08-470-220A-22
13	16	64.0	5	3	US-08-967-374-22
14	16	64.0	5	4	US-09-505-991-22
15	15	60.0	4	2	US-08-465-775-10
16	15	60.0	4	3	US-09-208-337-10
17	15	60.0	4	3	US-08-990-664-11
18	15	60.0	4	4	US-09-373-962-10
19	15	60.0	4	4	US-09-245-680-10
20	15	60.0	4	4	US-09-198-806C-10
21	15	60.0	4	4	US-09-352-191-10
22	15	60.0	4	4	US-09-012-400-10
23	15	60.0	4	4	US-09-264-563-10
24	15	60.0	5	1	US-08-079-812-53
25	15	60.0	5	2	US-08-082-847-6
26	15	60.0	5	2	US-08-637-759B-468
27	15	60.0	5	2	US-08-465-775-9

28	15	60.0	5	3	US-08-871-355A-468	Sequence 468, Appl
29	15	60.0	5	3	US-08-812-586-58	Sequence 58, Appl
30	15	60.0	5	3	US-09-208-337-9	Sequence 9, Appl
31	15	60.0	5	3	US-08-990-664-10	Sequence 10, Appl
32	15	60.0	5	4	US-09-373-962-9	Sequence 9, Appl
33	15	60.0	5	4	US-09-245-680-9	Sequence 9, Appl
34	15	60.0	5	4	US-09-198-806C-9	Sequence 9, Appl
35	15	60.0	5	4	US-09-352-191-9	Sequence 9, Appl
36	15	60.0	5	4	US-09-012-400-9	Sequence 9, Appl
37	15	60.0	5	4	US-09-201-945-468	Sequence 468, Appl
38	15	60.0	5	4	US-09-284-563-9	Sequence 9, Appl
39	15	60.0	6	1	US-08-079-812-52	Sequence 52, Appl
40	15	60.0	6	1	US-08-079-812-122	Sequence 122, Appl
41	15	60.0	6	1	US-08-082-847-4	Sequence 4, Appl
42	15	60.0	6	1	US-08-082-847-11	Sequence 11, Appl
43	15	60.0	6	1	US-08-082-847-13	Sequence 13, Appl
44	15	60.0	6	2	US-08-623-833B-26	Sequence 26, Appl
45	15	60.0	6	2	US-08-465-775-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-480-133A-15
; Sequence 15, Application US/08480133A
; Patent No. 5840691
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: McCarthy, James B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: Allen, Janice B.
; APPLICANT: Billups, Kevin L.
; APPLICANT: Everett, Jeffrey E.
; TITLE OF INVENTION: Method for Treating Inflammatory Diseases Using Polypeptides with Fibronectin Activity
; TITLE OF INVENTION: Method for Treating Inflammatory Diseases Using Polypeptides with Fibronectin Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5840691west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,133A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,903
; FILING DATE: 21-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,296
; FILING DATE: 10-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 600-308US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-480-133A-15

Query Match 72.0%; Score 18; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RARI 4
Db 1 RARI 4

RESULT 2
US-09-008-308-30
; Sequence 30, Application US/09008308
; Patent No. 6080575
; GENERAL INFORMATION:
; APPLICANT: Heidmann, Hans H.
; APPLICANT: Mueller, Rolf
; APPLICANT: Sedlacek, Hans-Harald
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
; TITLE OF INVENTION: ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES, AND
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,308
; FILING DATE: 16-JAN-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197 01 141.1
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-09-008-308-30

Query Match 72.0%; Score 18; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RARI 4
Db 1 RARI 4

RESULT 3
US-09-101-751A-57
; Sequence 57, Application US/09101751A
; Patent No. 6465253
; GENERAL INFORMATION:

; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS
; FILE REFERENCE: 85710
; CURRENT APPLICATION NUMBER: US/09/101,751A
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Description of Unknown Organism: Artificial
; OTHER INFORMATION: Sequence
US-09-101-751A-57

Query Match 72.0%; Score 18; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RARI 4
Db 2 RARI 5

RESULT 4
US-09-125-517A-42
; Sequence 42, Application US/09125517A
; Patent No. 6087336
; GENERAL INFORMATION:
; APPLICANT: Cotton, Ronald
; APPLICANT: Edwards, Philip Neil
; APPLICANT: Luke, Richard William Arthur
; TITLE OF INVENTION: Peptide Derivatives
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth St., N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,517A
; FILING DATE: 20-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9603855.9
; FILING DATE: 23-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9620819.4
; FILING DATE: 05-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377

```
;
; REFERENCE/DOCKET NUMBER: 1991-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-125-517A-42

Query Match 68.0%; Score 17; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RARI 4
Db 2 RARV 5

RESULT 5
US-09-284-625-6
; Sequence 6, Application US/09284625
; Patent No. 6207644
; GENERAL INFORMATION:
; APPLICANT: Luke, Richard William
; APPLICANT: Cotton, Richard
; TITLE OF INVENTION: Peptide Analogues Containing a 7-membered Lactam Ring
; FILE REFERENCE: 1991-169
; CURRENT APPLICATION NUMBER: US/09/284,625
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: PCT/GB97/02837
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: GB 96218367
; PRIOR FILING DATE: 1996-10-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PPT
; ORGANISM: Homo sapiens
; US-09-284-625-6

Query Match 68.0%; Score 17; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RARI 4
Db 2 RARV 5

RESULT 6
US-08-616-669A-57
; Sequence 57, Application US/08616669A
; Patent No. 5948765
; GENERAL INFORMATION:
; APPLICANT: Muslin, Anthony J.
; APPLICANT: Shaw, Andrew S.
; TITLE OF INVENTION: Inhibition of Intracellular Signal
; TRANSDUCTION BY 14-3-3-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Boulevard, Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: US
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/616,669A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Holland, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 964064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "A phosphorylated serine"
; US-08-616-669A-57

Query Match 68.0%; Score 17; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RARIY 5
Db 1 RSRXY 5

RESULT 7
US-09-125-517A-8
; Sequence 8, Application US/09125517A
; Patent No. 6087336
; GENERAL INFORMATION:
; APPLICANT: Cotton, Ronald
; APPLICANT: Edwards, Phillip Neil
; APPLICANT: Luke, Richard William Arthur
; TITLE OF INVENTION: Peptide Derivatives
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth St., N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,517A
; FILING DATE: 20-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9603855.9
; FILING DATE: 23-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9620819.4
; FILING DATE: 05-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1991-127
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "5-Phenylpentanoyl-Ala"
FEATURE:
NAME/KEY: Peptide
LOCATION: 6
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note=
OTHER INFORMATION: "[S]-2-((R)-3-amino-2-oxopyrrolidin-1-yl)propanoyl]-Gly-4-am

Query Match 68.0%; Score 17; DB 3; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RARI 4
DB 2 RARV 5

RESULT 8
US-09-326-440-57
Sequence 57, Application US/09326440
Patent No. 6207393
GENERAL INFORMATION:
APPLICANT: Muslin, Anthony J.
APPLICANT: Shaw, Andrew S.
TITLE OF INVENTION: Inhibition of Intracellular Signal
TITLE OF INVENTION: Transduction by 14-3-3-Binding Peptides
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Boulevard, Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: US
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/326,440
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/616,669
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Holland, Donald R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 964064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "A phosphorylated serine"
US-09-326-440-57

Query Match 68.0%; Score 17; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RARIY 5
DB 1 RSRXY 5

RESULT 9
US-09-057-052-7
Sequence 7, Application US/09057052
Patent No. 6331422
GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.
APPLICANT: Schense, Jason
TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for
TITLE OF INVENTION: Tissue Engineering
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins L.L.P.
STREET: 600 Congress Avenue, Suite 2700
CITY: Austin
STATE: Texas
COUNTRY: US
ZIP: 78701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,052
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,143
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: CAL430.23000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 495-8400
TELEFAX: (512) 495-8612
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-057-052-7

Query Match 68.0%; Score 17; DB 4; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RARI 4
DB 3 RARV 6

RESULT 10
US-09-008-308-29
Sequence 29, Application US/09008308

```

; Patent No. 6080575
; GENERAL INFORMATION:
; APPLICANT: Heilmann, Hans H.
; APPLICANT: Mueller, Rolf
; APPLICANT: Sedlacek, Hans-Harald
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
; TITLE OF INVENTION: ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES, AND
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,308
; FILING DATE: 16-JAN-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197 01 141.1
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0189
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal
; US-09-008-308-29

Query Match 64.0%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RARI 4
Db 1 RARL 4

RESULT 11
US-08-095-162-22
; Sequence 22, Application US/08095162
; Patent No. 5512459
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Stout, Jay
; APPLICANT: Henriksen, Dennis
; APPLICANT: Partridge, Bruce
; APPLICANT: Manning, Shane
; TITLE OF INVENTION: Enzymatic Method for Modification of
; TITLE OF INVENTION: Recombinant Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5512459west Center
; CITY: Minneapolis
; STATE: MN

; Patent No. 6080575
; GENERAL INFORMATION:
; APPLICANT: Heilmann, Hans H.
; APPLICANT: Mueller, Rolf
; APPLICANT: Sedlacek, Hans-Harald
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
; TITLE OF INVENTION: ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES, AND
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,308
; FILING DATE: 16-JAN-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197 01 141.1
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0189
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal
; US-09-008-308-29

Query Match 64.0%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RARI 4
Db 1 RARL 4

RESULT 11
US-08-095-162-22
; Sequence 22, Application US/08095162
; Patent No. 5512459
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Stout, Jay
; APPLICANT: Henriksen, Dennis
; APPLICANT: Partridge, Bruce
; APPLICANT: Manning, Shane
; TITLE OF INVENTION: Enzymatic Method for Modification of
; TITLE OF INVENTION: Recombinant Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5512459west Center
; CITY: Minneapolis
; STATE: MN

; Patent No. 6080575
; GENERAL INFORMATION:
; APPLICANT: Heilmann, Hans H.
; APPLICANT: Mueller, Rolf
; APPLICANT: Sedlacek, Hans-Harald
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
; TITLE OF INVENTION: ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES, AND
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,308
; FILING DATE: 16-JAN-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197 01 141.1
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0189
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal
; US-09-008-308-29

Query Match 64.0%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RARI 4
Db 1 RARL 4

RESULT 12
US-08-470-220A-22
; Sequence 22, Application US/08470220A
; Patent No. 5707826
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Stout, Jay
; APPLICANT: Henriksen, Dennis
; APPLICANT: Partridge, Bruce
; APPLICANT: Manning, Shane
; TITLE OF INVENTION: Enzymatic Method for Modification of
; TITLE OF INVENTION: Recombinant Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5707826west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,220A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/095,162
; FILING DATE: 20-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,659
; REFERENCE/DOCKET NUMBER: 8648.32-US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
```

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; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,162
; FILING DATE: 20-JUL-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,659
; REFERENCE/DOCKET NUMBER: 8648.32-US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-095-162-22

Query Match 64.0%; Score 16; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RARI 4
Db 1 RARL 4

RESULT 12
US-08-470-220A-22
; Sequence 22, Application US/08470220A
; Patent No. 5707826
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Stout, Jay
; APPLICANT: Henriksen, Dennis
; APPLICANT: Partridge, Bruce
; APPLICANT: Manning, Shane
; TITLE OF INVENTION: Enzymatic Method for Modification of
; TITLE OF INVENTION: Recombinant Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5707826west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,220A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/095,162
; FILING DATE: 20-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,659
; REFERENCE/DOCKET NUMBER: 8648.32-US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
```

TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-470-220A-22

Query Match 64.0%; Score 16; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 1 RARI 4
; |||
Db 1 RARL 4

RESULT 13

US-08-967-374-22

; Sequence 22, Application US/08967374

; Patent No. 6037143

; GENERAL INFORMATION:

; APPLICANT: Wagner, Fred W.

; APPLICANT: Stout, Jay

; APPLICANT: Henriksen, Dennis

; APPLICANT: Partridge, Bruce

; APPLICANT: Manning, Shane

; TITLE OF INVENTION: Enzymatic Method for Modification of

; RECOMBINANT POLYPEPTIDES

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merchant & Gould

; STREET: 3100 No. 6037143 West Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/967,374

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/520,485

; FILING DATE: 29-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Carter, Charles G.

; REGISTRATION NUMBER: 35,093

; REFERENCE/DOCKET NUMBER: 8648.32-US01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-332-5300

; TELEFAX: 612-332-9081

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-967-374-22

Query Match 64.0%; Score 16; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 1 RARI 4
; |||
Db 1 RARL 4

RESULT 14

US-09-505-991-22

; Sequence 22, Application US/09505991

; Patent No. 6403361

; GENERAL INFORMATION:

; APPLICANT: Wagner, Fred W.

; Stout, Jay

; Henriksen, Dennis

; Partridge, Bruce

; Manning, Shane

; TITLE OF INVENTION: Enzymatic Method for Modification of

; RECOMBINANT POLYPEPTIDES

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merchant & Gould

; STREET: 3100 No. 6403361 West Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/505,991

; FILING DATE: 17-Feb-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/520,485

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Carter, Charles G.

; REGISTRATION NUMBER: 35,093

; REFERENCE/DOCKET NUMBER: 8648.32-US01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-332-5300

; TELEFAX: 612-332-9081

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: Peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-505-991-22

Query Match 64.0%; Score 16; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RARI 4
; |||
Db 1 RARL 4

RESULT 15

US-08-465-775-10

; Sequence 10, Application US/08465775

; Patent No. 5955430

; GENERAL INFORMATION:

; APPLICANT: Rodgers, Kathleen E.

; APPLICANT: dizerega, Gere S.

; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND

; ANALOGS THEREOF IN TISSUE REPAIR

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: c/o Robbins, Berliner & Carson

; STREET: 201 No. 5955430th Figueroa Street #500

; CITY: Los Angeles

; STATE: CA

;; COUNTRY: USA
;; ZIP: 90012
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/465,775
;; FILING DATE:
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Spitals, John P.
;; REGISTRATION NUMBER: 29,215
;; REFERENCE/DOCKET NUMBER: 1920-360
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 977-1001
;; TELEFAX: (213) 977-1003
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-465-775-10

Query Match 60.0%; Score 15; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 RY 5
Db 2 RY 4

Search completed: December 12, 2002, 15:20:53
Job time : 9.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2002, 15:17:24 ; Search time 5.25 Seconds
(without alignments)
15.869 Million cell updates/sec

Title: US-09-600-432-25

Perfect score: 25

Sequence: 1 RARI 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105981 seqs, 16662342 residues

Total number of hits satisfying chosen parameters: 5573

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
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 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	72.0	4	10	US-09-010-714-10
2	17	68.0	6	9	US-10-024-918-7
3	17	68.0	6	10	US-09-887-469-20
4	16	64.0	4	8	US-08-484-409-24
5	15	60.0	4	9	US-09-900-936-10
6	15	60.0	4	10	US-09-771-192-10
7	15	60.0	4	10	US-09-837-697A-10
8	15	60.0	5	9	US-09-900-936-9
9	15	60.0	5	10	US-09-771-192-9
10	15	60.0	5	10	US-09-837-697A-9
11	15	60.0	6	9	US-09-900-936-5
12	15	60.0	6	9	US-09-900-936-8
13	15	60.0	6	10	US-09-771-192-8
14	15	60.0	6	10	US-09-771-192-5
15	15	60.0	6	10	US-09-837-697A-5
16	15	60.0	6	10	US-09-837-697A-8
17	14	56.0	5	10	US-09-800-433-5
18	14	56.0	5	10	US-09-800-433-7
19	14	56.0	5	10	US-09-977-831-19

20	14	56.0	5	10	US-09-947-387-47	Sequence 47, Appl
21	14	56.0	6	9	US-09-823-823-66	Sequence 66, Appl
22	14	56.0	6	10	US-09-904-599A-3	Sequence 3, Appl
23	14	56.0	6	10	US-09-823-823-66	Sequence 31, Appl
24	13	52.0	4	8	US-08-484-409-31	Sequence 66, Appl
25	13	52.0	4	12	US-10-041-030-25	Sequence 25, Appl
26	13	52.0	5	9	US-10-104-019-43	Sequence 43, Appl
27	13	52.0	5	10	US-09-748-114-28	Sequence 28, Appl
28	12	48.0	4	10	US-09-947-387-48	Sequence 48, Appl
29	12	48.0	5	10	US-09-817-661-28	Sequence 28, Appl
30	12	48.0	5	10	US-09-977-831-26	Sequence 26, Appl
31	12	48.0	5	10	US-09-947-387-92	Sequence 26, Appl
32	12	48.0	5	10	US-09-947-387-127	Sequence 92, Appl
33	12	48.0	5	10	US-09-071-838-266	Sequence 266, App
34	12	48.0	6	9	US-09-981-876-277	Sequence 277, App
35	12	48.0	6	9	US-09-813-718-44	Sequence 44, Appl
36	12	48.0	6	10	US-09-202-077-8	Sequence 8, Appl
37	12	48.0	6	10	US-09-947-387-91	Sequence 91, Appl
38	12	48.0	6	10	US-09-947-387-118	Sequence 118, App
39	12	48.0	6	10	US-09-911-838-62	Sequence 62, Appl
40	12	48.0	6	10	US-09-911-838-64	Sequence 64, Appl
41	12	48.0	6	10	US-09-911-838-66	Sequence 66, Appl
42	12	48.0	6	12	US-10-156-820-45	Sequence 45, Appl
43	12	48.0	6	12	US-10-156-820-76	Sequence 76, Appl
44	11	44.0	4	9	US-09-841-730-22	Sequence 22, Appl
45	11	44.0	4	9	US-09-859-211-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-010-714-10
; Sequence 10, Application US/09010714
; Patent No. US2002012942A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo I.
; APPLICANT: Iida, Joji
; TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
; FILE REFERENCE: 600.332US01
; CURRENT APPLICATION NUMBER: US/09/010,714
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-010-714-10

Query Match 72.0%; Score 18; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RARI 4
DB 1 RARI 4

RESULT 2
US-10-024-918-7
; Sequence 7, Application US/10024918
; Patent No. US20020168718A1
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey
; APPLICANT: Schense, Jason
; APPLICANT: Zisch, Andreas
; APPLICANT: Hall, Heike
; TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
; FILE REFERENCE: CIT 2606 CIP
; CURRENT APPLICATION NUMBER: US/10/024,918

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; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heparin-binding sequence from fibronectin
US-10-024-918-7

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Query Match      68.0%; Score 17; DB 9; Length 6;
Best Local Similarity 75.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RARI 4
    |||
Db 3 RARV 6

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RESULT 3
US-09-887-469-20
; Sequence 20, Application US/09887469
; Patent No. US20020146433A1
; GENERAL INFORMATION:
; APPLICANT: Krempf, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; FILE OF INVENTION: PROTECTIVE ANTIGENS FROM PROMOTOR-PROXIMAL-GENES
; FILE REFERENCE: 15280-424-1US
; CURRENT APPLICATION NUMBER: US/09/887,469
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Respiratory Syncytial Virus
US-09-887-469-20

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Query Match      68.0%; Score 17; DB 10; Length 6;
Best Local Similarity 75.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 RARI 4
    |||
Db 1 RARV 4

```

```

RESULT 4
US-08-484-409-24
; Sequence 24, Application US/08484409
; Patent No. US20020076412A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Zamvil, Scott
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,409
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.409C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-484-409-24

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Query Match      64.0%; Score 16; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 3 RIV 5
    |||
Db 1 RIV 3

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```

RESULT 5
US-09-900-936-10
; Sequence 10, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE OF INVENTION: or Differentiation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-900-936-10

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```

Query Match      60.0%; Score 15; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 3 RIV 5
    |||
Db 2 RIV 4

```

```

RESULT 6
US-09-771-192-10
; Sequence 10, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A

```

```

; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-771-192-10

Query Match          60.0%; Score 15; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RY 5
   | |
Db 2 RY 4

RESULT 7
US-09-837-697A-10
; Sequence 10, Application US/09837697A
; Patent No. US20020146823A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rogers, Kathleen E.
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
; TITLE OF INVENTION: Differentiation
; FILE REFERENCE: 97,017-F1A
; CURRENT APPLICATION NUMBER: US/09/837,697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: AII(1-4)
US-09-837-697A-10

Query Match          60.0%; Score 15; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RY 5
   | |
Db 2 RY 4

RESULT 8
US-09-900-936-9
; Sequence 9, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; TITLE OF INVENTION: or Differentiation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)

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US-09-900-936-9
Query Match          60.0%; Score 15; DB 9; Length 5;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RY 5
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Db 2 RY 4

RESULT 9
US-09-771-192-9
; Sequence 9, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)
US-09-771-192-9

Query Match          60.0%; Score 15; DB 10; Length 5;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RY 5
   | |
Db 2 RY 4

RESULT 10
US-09-837-697A-9
; Sequence 9, Application US/09837697A
; Patent No. US20020146823A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rogers, Kathleen E.
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Prolif
; TITLE OF INVENTION: Differentiation
; FILE REFERENCE: 97,017-F1A
; CURRENT APPLICATION NUMBER: US/09/837,697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: AII(1-5)
US-09-837-697A-9

Query Match          60.0%; Score 15; DB 10; Length 5;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RY 5
   | |
Db 2 RY 4

```

```
RESULT 11
US-09-900-936-5
; Sequence 5, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: digerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (2-7)
US-09-900-936-5
Query Match 60.0%; Score 15; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 RY 5
Db 1 RY 3
RESULT 12
US-09-900-936-8
; Sequence 8, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: digerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)
US-09-900-936-8
Query Match 60.0%; Score 15; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 RY 5
Db 1 RY 3
RESULT 13
US-09-771-192-5
; Sequence 5, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: digerega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (2-7)
US-09-771-192-5
Query Match 60.0%; Score 15; DB 10; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 RY 5
Db 1 RY 3
RESULT 14
US-09-771-192-8
; Sequence 8, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: digerega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)
US-09-771-192-8
Query Match 60.0%; Score 15; DB 10; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 RY 5
Db 2 RY 4
RESULT 15
US-09-837-697A-5
; Sequence 5, Application US/09837697A
; Patent No. US20020146823A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rogers, Kathleen E.
; APPLICANT: digerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Prolif
; FILE REFERENCE: 97,017-F1A
; CURRENT APPLICATION NUMBER: US/09/837,697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: AII(2-7)
US-09-837-697A-5
Query Match 60.0%; Score 15; DB 10; Length 6;
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Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RY 5
|:
Db 1 RY 3

Search completed: December 12, 2002, 15:21:20
Job time : 5.25 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:58 ; Search time 11 Seconds
(without alignments)
43.697 Million cell updates/sec

Title: US-09-600-432-25

Perfect score: 25

Sequence: 1 RARIY 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	13	52.0	5	S62883	seminal plasma protein
2	11	44.0	4	PT0721	T-cell receptor beta
3	11	44.0	5	JT0870	phycocyanin-like
4	10	40.0	6	JN0861	peptidyl-dipeptidase
5	10	40.0	6	AI1490	pyruvate kinase (E
6	10	40.0	6	I49421	laminin B1 - weste
7	9	36.0	4	I61883	protamine p1 - ora
8	9	36.0	4	I37013	protamine p1 - Cor
9	9	36.0	4	I84439	protamine p1 - sav
10	9	36.0	5	I40702	primase - Citrobac
11	9	36.0	5	I39964	ribosomal protein
12	9	36.0	5	I39966	ribosomal protein
13	9	36.0	5	I39965	ribosomal protein
14	9	36.0	5	PQ0009	angiotensin-conver
15	9	36.0	6	I37027	hypothetical 6 pro
16	9	36.0	6	I37027	hypothetical 6 pro
17	9	36.0	6	B33932	protamine p1 - gor
18	9	36.0	6	PT0518	Ig mu chain D regi
19	9	36.0	6	PT0568	T-cell receptor be
20	7	28.0	3	A22565	R-phycocyanin al
21	7	28.0	3	A43391	TRH-like tripeptid
22	7	28.0	3	S68328	blood cell protein
23	7	28.0	4	A32039	tyrosine-melanocyt
24	7	28.0	4	A37832	phenol 2-monooxye
25	7	28.0	4	S09478	globulin IV alpha
26	7	28.0	4	PT0240	Ig heavy chain CRD
27	7	28.0	4	S43959	Ig mu chain V regi
28	7	28.0	4	PT0697	T-cell receptor be
29	7	28.0	5	H0ROHA	proctolin - Americ

30	7	28.0	5	B37325	pap fibrial regul
31	7	28.0	5	I40469	dnax-like protein
32	7	28.0	5	E60274	major protein anti
33	7	28.0	5	F22565	R-phycocyanin ga
34	7	28.0	5	PQ0689	photosystem I 10.4
35	7	28.0	5	B61445	Leu-enkephalin - b
36	7	28.0	5	A61445	Met-enkephalin - b
37	7	28.0	5	A60411	proctolin - Atlant
38	7	28.0	5	S53595	hypothetical prote
39	7	28.0	5	PT0278	Ig heavy chain CRD
40	7	28.0	5	PT0295	Ig heavy chain CRD
41	7	28.0	5	S68326	blood cell protein
42	7	28.0	6	S04617	alcohol dehydrogen
43	7	28.0	6	A61411	ameletin - rat
44	7	28.0	6	S11556	hydrogensulfite re
45	7	28.0	6	B44510	hypothetical prote

ALIGNMENTS

RESULT 1

S62883

seminal plasma protein II - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S62883

R:Romero, A.; Varela, P.F.; Sanz, L.; Toepfer-Petersen, E.; Calvete, J.J.

FEBS Lett. 382, 15-17, 1996

A:Title: Crystallization and preliminary X-ray diffraction analysis of boar seminal p

A:Reference number: S62882; MUID:96196555; PMID:8612739

A:Accession: S62883

A:Molecule type: protein

A:Residues: 1-5 <RQ>

C:Complex: heterodimer; seminal plasma protein I and seminal plasma protein II

C:Keywords: glycoprotein; heterodimer; semen

Query Match 52.0%; Score 13; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ARI 4

Db 1 ARI 3

RESULT 2

PT0721

T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0721

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0721

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 44.0%; Score 11; DB 2; Length 4;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ARI 4

Db 1 ARI 3

RESULT 3

```
JT0870
Phytosulfokine alpha - garden asparagus (fragment)
C:Species: Asparagus officinalis (garden asparagus)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 19-Apr-2002
C:Accession: JT0870
R:Matubayashi, Y.; Sakagami, Y.
Proc. Natl. Acad. Sci. U.S.A. 93, 7623-7627, 1996
A:Title: Phytosulfokine sulfated peptides that induce the proliferation of single mesophyll cells
A:Reference number: JT0870
A:Accession: JT0870
A:Molecule type: protein
A:Residues: 1-5 <MAT>

Query Match 44.0%; Score 11; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IY 5
DB 2 IY 3

RESULT 4
JN0861
peptidyl-dipeptidase A inhibitory peptide C111 - striped bonito
C:Species: Sarda orientalis (striped bonito)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: JN0861
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide
A:Reference number: JN0859; MUID:94080036; PMID:7764272
A:Accession: JN0861
A:Molecule type: protein
A:Residues: 1-6 <MAT>
A:Experimental source: liver
C:Comment: The carboxyl end is essential for the protein's expression of angiotensin I-converting enzyme inhibitor
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 40.0%; Score 10; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IY 5
DB 2 IY 3

RESULT 5
A11490
pyruvate kinase (EC 2.7.1.40) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Mar-1995
C:Accession: A11490
R:Hjeltnist, G.; Andersson, J.; Edlund, B.; Engstrom, L.
Biochem. Biophys. Res. Commun. 61, 559-563, 1974
A:Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate kinase phosphorylated in vitro
A:Reference number: A11490; MUID:75127438; PMID:4375989
A:Accession: A11490
A:Molecule type: protein
A:Residues: 1-6 <HJE>
A:Experimental source: liver
C:Keywords: glycolysis; phosphotransferase

Query Match 40.0%; Score 10; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RARI 4
DB 3 RASL 6
```

```
RESULT 6
I49421
laminin B1 - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49421
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829

Query Match 40.0%; Score 10; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IY 5
DB 1 IY 2

RESULT 7
I61883
protamine p1 - orangutan (fragment)
C:Species: Pongo pygmaeus (orangutan)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: I61883
R:Queraut, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-A
A:Reference number: I37013; MUID:94040810; PMID:8224908
A:Accession: I61883
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12146; NID:g38156; PIDN:CAA78130.1; PID:g4379372

Query Match 36.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AR 3
DB 2 AR 3

RESULT 8
I37013
protamine p1 - Cercopithecus patas (fragment)
C:Species: Cercopithecus patas
C:Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I37013
R:Queraut, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-A
A:Reference number: I37013; MUID:94040810; PMID:8224908
A:Accession: I37013
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12150; NID:g22814; PIDN:CAA78134.1; PID:g4377415

Query Match 36.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AR 3
DB 2 AR 3
```

Db 2 AR 3

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AR 3
||
Db 2 AR 3

RESULT 9
I84439
protamine P1 - savannah baboon (fragment)
C:Species: Papio hamadryas doquera (savannah baboon)
C:Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I84439
R:Queralt, R.; Oliva, R.
Gene I33, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810; PMID:8224908
A:Accession: I84439
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:212147; NID:g38134; PIDN:CAA78131.1; PID:g4379349

Query Match 36.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AR 3
||
Db 2 AR 3

RESULT 10
I40702
primase - Citrobacter diversus (fragment)
C:Species: Citrobacter diversus
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Aug-1996
C:Accession: I40702
R:Versalovic, J.; Lupski, J.R.
Mol. Microbiol. 8, 343-355, 1993
A:Title: Conservation and evolution of the rpsU-dnaG-rpoD macromolecular synthesis (MMS)
A:Reference number: I40702; MUID:93302510; PMID:8316085
A:Accession: I40702
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:L01754; NID:gl44439
C:Genetics:
A:Gene: dnaG

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RI 4
||
Db 4 RI 5

RESULT 11
I39964
ribosomal protein S4 - Bacillus circulans (fragment)
C:Species: Bacillus circulans
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39964
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
A:Accession: I39964
A>Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99041; NID:gl43471
C:Genetics:
A:Gene: rpsD

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AR 3
||
Db 2 AR 3

RESULT 12
I39966
ribosomal protein S4 - Bacillus licheniformis (fragment)
C:Species: Bacillus licheniformis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39966
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
A:Accession: I39966
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99043; NID:gl43475
C:Genetics:
A:Gene: rpsD

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AR 3
||
Db 2 AR 3

RESULT 13
I39965
ribosomal protein S4 - Bacillus megaterium (fragment)
C:Species: Bacillus megaterium
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39965
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
A:Accession: I39965
A>Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99042; NID:gl43473
C:Genetics:
A:Gene: rpsD

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AR 3
||
Db 2 AR 3

RESULT 14
PQ0009
angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N:Alternate names: ficus latex peptide 2
C:Species: Ficus carica (common fig)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C:Accession: PQ0009
R:Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A;Reference number: PQ0008
A;Accession: PQ0009
A;Molecule type: protein
A;Residues: 1-5 <MAR>
A;Experimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 IY 5
Db 1 LY 2

RESULT 15

PC4127
hypothetical 6 protein - Streptomyces clavuligerus (fragment)
C;Species: Streptomyces clavuligerus
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PC4127
R;Rodriguez-Garcia, A.; Martin, J.F.; Liras, P.
Gene 167, 9-15, 1995
A;Title: The argG gene of Streptomyces clavuligerus has low homology to unstable argG fr
A;Reference number: JC4548; MUID:96144242; PMID:8566818
A;Accession: PC4127
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6 <ROD>
A;Cross-references: EMBL:249111

Query Match 36.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RA 2
Db 5 RA 6

Search completed: December 12, 2002, 15:20:08
Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:38 ; Search time 6 Seconds
(without alignments)
34.564 Million cell updates/sec

Title: US-09-600-432-25

Perfect score: 25

Sequence: 1 RARIY 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	44.0	5	1 PSK_DAUCA	P58261 daucus caro
2	9	36.0	4	1 FYRI_ANCEL	P58706 anthopleura
3	8	32.0	6	1 UN06_CLOPA	P81351 clostridium
4	7	28.0	4	1 FAR3_HIRME	P42562 hirudo medi
5	7	28.0	4	1 FAR4_HIRME	P42563 hirudo medi
6	7	28.0	5	1 AL14_CARMA	P81817 carcinus ma
7	7	28.0	5	1 FARP_ARTTR	P41853 artiposthi
8	7	28.0	5	1 PRCT_PERAM	P01373 periplaneta
9	7	28.0	5	1 UC22_MAIZE	P80628 zea mays (m
10	7	28.0	6	1 ASP2_LACSN	P82655 lactobacill
11	7	28.0	6	1 OYML_LFDE	P42385 leptonotars
12	6	24.0	4	1 DCMS_PSECH	P19318 pseudomonas
13	6	24.0	4	1 FFKA_ANCEL	P58705 anthopleura
14	6	24.0	4	1 TUFT_HUMAN	P01858 homo sapien
15	6	24.0	6	1 CIP2_MYTED	P13737 mytilus edu
16	6	24.0	6	1 EI01_LITRU	P82096 litorea rub
17	5	20.0	4	1 FLRF_HIRME	P42561 hirudo medi
18	5	20.0	4	1 FLRN_ANCEL	P58707 anthopleura
19	5	20.0	4	1 FMRF_MACNI	P01162 macrocallis
20	5	20.0	5	1 EI03_LITRU	P82099 litorea rub
21	5	20.0	5	1 EI04_LITRU	P82100 litorea rub
22	5	20.0	5	1 UF01_MOUSE	P38639 mus musculu
23	5	20.0	6	1 ACPR_RABIT	P25154 cryotolagus
24	5	20.0	6	1 FARP_MONEX	P41966 monilezia ex
25	4	16.0	3	1 LUXE_VIBFI	P24272 vibrio fisc
26	4	16.0	4	1 ACHI_ACHFU	P35904 achatina fu
27	4	16.0	5	1 BIOB_CITFR	P12997 citrobacter
28	4	16.0	5	1 BPP7_BOTIN	P30425 bothrops in
29	4	16.0	5	1 RE11_LITRU	P82070 litorea rub
30	4	16.0	5	1 RE21_LITRU	P82071 litorea rub
31	4	16.0	5	1 RE31_LITRU	P82072 litorea rub
32	4	16.0	5	1 SUGA_ACHDO	P19991 achneta dome
33	4	16.0	6	1 CIP1_MYTED	P13736 mytilus edu

34	4	16.0	6	1 LOK1_LOCMI	P41491 locusta mig
35	4	16.0	6	1 TMOF_SARBU	P41495 sarcophaga
36	4	16.0	6	1 TRPI_PSEPU	P36414 pseudomonas
37	3	12.0	4	1 EOST_HUMAN	P02731 homo sapien
38	3	12.0	4	1 OCPI_OCTMI	P58648 octopus min
39	3	12.0	4	1 RM01_YEAST	P36515 saccharomyc
40	3	12.0	5	1 PAP2_PARMA	P81864 pardachirus
41	3	12.0	5	1 RE32_LITRU	P82073 litorea rub
42	3	12.0	5	1 TPIS_CANPA	P54714 canis famli
43	2	8.0	3	1 GRWM_HUMAN	P01157 homo sapien
44	2	8.0	3	1 THYL_PIG	P01151 sus scrofa
45	2	8.0	4	1 DCML_PSECH	P19916 pseudomonas

ALIGNMENTS

RESULT 1
PSK_DAUCA
ID PSK_DAUCA STANDARD; PRT; 5 AA.
AC P58261;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
DE beta)].
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC STRAIN=cv. US-Harumakigosun;
RX MEDLINE=2012743; PubMed=10750705;
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
RA Kanada H., Sakagami Y.;
RT "A secreted peptide growth factor, phytosulfokine, acting as a
stimulatory factor of carrot somatic embryo formation.";
RL Plant Cell Physiol 41:27-32(2000).
CC -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
EMBRYOS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
FT MOD_RES 1 1 SULFATION.
FT MOD_RES 3 3 SULFATION.
SQ SEQUENCE 5 AA; 687 MW; 76C1B504B500000 CRC64;

Query Match 44.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 IY 5
Db 2 IY 3

RESULT 2
FYRI_ANCEL
ID FYRI_ANCEL STANDARD; PRT; 4 AA.
AC P58706;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antho-Riamide I [Contains: Antho-Riamide II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthae; Actinillidae; Anthopleura.

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OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270459; PubMed=1821096;
RA Notherack H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
RT des-phenyllactyl fragment Tyr-Arg-Ile-NH2."
RL Peptides 12:1165-1173(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Notherack H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kamide and Antho-Riamide."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -|- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Neuron-specific.
DR InterPro: IPR001023; Hsp70.
KW Neuropeptide; Amidation.
FT CHAIN 1 4 ANTHO-RIAMIDE I.
FT CHAIN 2 4 ANTHO-RIAMIDE II.
FT CHAIN 3 1 L-3-PHENYLACTYL.
FT MOD_RES 1 1 AMIDATION.
FT MOD_RES 4 4 AMIDATION.
FT SEQUENCE 4 AA; 598 MW; 60441B99A000000000 CRC64;

Query Match 36.0%; Score 9; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RI 4
DB 3 RI 4

RESULT 3
ID UN06_CLOPA STANDARD; PRT; 6 AA.
AC P81351.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Unknown protein CP 6 from 2D-page (fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RX STRAIN=W5;
RC MEDLINE=98291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 75.9 KDa.
FT NON_TER 6 6
FT SEQUENCE 6 AA; 657 MW; 605B1DC1A5A80000 CRC64;

Query Match 32.0%; Score 8; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARI 4
DB 4 AEI 6

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RESULT 4
ID FAR3_HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YLRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4 AMIDATION.
FT SEQUENCE 4 AA; 598 MW; 69D4073B3000000000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 Y 5
DB 1 Y 1

RESULT 5
ID FAR4_HIRME STANDARD; PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4 AMIDATION.
FT SEQUENCE 4 AA; 616 MW; 69D4068B3000000000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 Y 5
DB 1 Y 1

RESULT 6
ID AL14_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

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DE Carcinustatin 14.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubranchyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -|- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -|- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 5 5 AMIDATION (POTENTIAL).
 SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 Y 5
 Db 1 Y 1

RESULT 7
 FARP_ARTTR STANDARD; PRT; 5 AA.
 AC P41853;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide RYRF-amide.
 OS Artroposthia triangulata.
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
 OC Terricola; Geoplanidae; Arthurdendyus.
 OX NCBI_TaxID=132421;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=94211927; PubMed=7909164;
 RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
 RT "RYRFamide: a turbellarian FMRFamide-related peptide (FARP).";
 RL Regul. Pept. 50:37-43(1994).
 CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC -|- FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 5 5 AMIDATION.
 FT MOD_RES 5 5
 SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 Y 5
 Db 2 Y 2

RESULT 8
 PRCY_PERAM STANDARD; PRT; 5 AA.
 AC P01373;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Proctolin.
 OS Periplaneta americana (American cockroach), and
 OS Limulus polyphemus (Atlantic horseshoe crab), and

OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattellidae; Periplaneta.
 OX NCBI_TaxID=6978, 6850, 6759;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=76074708; PubMed=576;
 RA Starratt A.N., Brown B.E.;
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
 RT in insects.";
 RL Life Sci. 17:1253-1256(1975).
 RN [2]
 RP BIOLOGICAL SOURCE.
 RC SPECIES=P.americana;
 RX MEDLINE=81225865; PubMed=6113690;
 RA O'Shea M., Adams M.E.;
 RT "Pentapeptide (proctolin) associated with an identified neuron.";
 RL Science 213:567-569(1981).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.polyphemus;
 RX MEDLINE=90287800; PubMed=2356151;
 RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shabanowitz J.;
 RT "Identification of proctolin in the central nervous system of the
 RT horseshoe crab, Limulus polyphemus.";
 RL Peptides 11:205-211(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=C.maenas;
 RX MEDLINE=86232789; PubMed=2872661;
 RA Stangler J., Birksen H., Keller R.;
 RT "Identification and immunocytochemical localization of proctolin in
 RT pericardial organs of the shore crab, Carcinus maenas.";
 RL Peptides 7:67-72(1986).
 CC -|- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
 CC -|- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.
 DR PIR; A01644; HOROHA.
 DR PIR; A60411; A60411.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 Y 5
 Db 2 Y 2

RESULT 9
 UC22_MAIZE STANDARD; PRT; 5 AA.
 ID UC22_MAIZE
 AC P80628;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
 DE (Fragment).
 DE Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;

RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
 DR Maize-2DPAGE; P80628; COLEOPTILE.
 DR MaizeDB; 123954; -.
 FT NON_TER 1 1
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA: 654 MW; 72CB19C9C0300000 CRC64;
 Query Match 28.0%; Score 7; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 IY 5
 Db 1 IF 2

RESULT 10
 ID ASP2_LACSN STANDARD; PRT; 6 AA.
 AC P82655;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acid shock protein 2 (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 CC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 CC Lactobacillus.
 OX NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CB1;
 RX MEDLINE=21322712; PubMed=11429463;
 RA De Angelis M., Bini L., Pallini V., Coconcelli P.S., Cobbetti M.;
 RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
 RL Microbiology 147:1863-1873(2001).
 CC -1- INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.
 FT NON_TER 6
 SQ SEQUENCE 6 AA: 778 MW; 6AA45B5B132A8000 CRC64;
 Query Match 28.0%; Score 7; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 Y 5
 Db 4 Y 4

RESULT 11
 ID OVA_LEPDE STANDARD; PRT; 6 AA.
 AC P42985;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Oviductal motility stimulating peptide (LeD-OVM).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Cucujiformia; Phycophaga; Chrysomelidae; Chrysomelidae;
 CC Chrysomelinae; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=91271080; PubMed=2052497;
 RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,

RA Proost P., Torrekens S., de Loof A.;
 RT "Isolation, identification and synthesis of novel oviductal motility
 RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
 RT decemlineata.";
 RL Peptides 12:31-36(1991).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 CC Neuropeptide; Amidation.
 KW MOD_RES 6
 FT NON_TER 6
 FT NON_TER 6
 SQ SEQUENCE 6 AA: 720 MW; 6B07632B5DD03000 CRC64;
 Query Match 28.0%; Score 7; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 Y 5
 Db 3 Y 3

RESULT 12
 ID DCMS_PSECH STANDARD; PRT; 4 AA.
 AC P19918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit S) (CO-DH S) (Fragment).
 GN CUTS.
 OS Pseudomonas carboxydohydrogena.
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Bradyrhizobium group.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydohydrogenic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -1- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 CC PIR: P10146; P10146.
 KW Oxidoreductase; Iron-sulfur.
 FT NON_TER 4
 FT NON_TER 4
 SQ SEQUENCE 4 AA: 420 MW; 6DD33DD6F0000000 CRC64;
 Query Match 24.0%; Score 6; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AR 3
 Db 2 AK 3

RESULT 13
 ID FFKA_ATEL STANDARD; PRT; 4 AA.
 AC P58705;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Antho-KAamide.
 CC Anthopleura elegantissima (Sea anemone).
 CC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 CC Nynanthae; Actiniidae; Anthopleura.


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OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Nothern H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenylacetyl-Phe-Lys-Ala-NH2 (Antho-Kamide), a
RL novel neuropeptide from sea anemones.";
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothern H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RL inhibitory neuropeptides, Antho-Kamide and Antho-Ramide.";
RL Proc. R. Soc. Lond. B. Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339CA00000000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RA 2
   :|
DB 3 KA 4

RESULT 14
TUFT_HUMAN
ID TUFT_HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
RL stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
RT activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
CC ACTIVITY OF NEUTROPHILS.
DR PIR; A02147; A02147.
DR MIM; 191150; -.
SQ SEQUENCE 4 AA; 501 MW; 74176321C00000000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 4;
Best Local Similarity 33.3%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Nothern H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenylacetyl-Phe-Lys-Ala-NH2 (Antho-Kamide), a
RL novel neuropeptide from sea anemones.";
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothern H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RL inhibitory neuropeptides, Antho-Kamide and Antho-Ramide.";
RL Proc. R. Soc. Lond. B. Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339CA00000000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RA 2
   :|
DB 3 KA 4

RESULT 15
CIP2_MYTED
ID CIP2_MYTED STANDARD; PRT; 6 AA.
AC P13737;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide II (MIP II).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloida; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
CC MUSCLES.
CC -!- SIMILARITY: TO MIP I.
DR PIR; B27696; B27696.
KW Hormone; Amidation.
FT MOD_RES 6 6 AMIDATION.
SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 6;
Best Local Similarity 25.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARIY 5
   |::
DB 2 APMF 5

Search completed: December 12, 2002, 15:19:17
Job time : 6 secs
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:09:54 ; Search time 21.25 Seconds
(without alignments)
48.482 Million cell updates/sec

Title: US-09-600-432-25

Perfect score: 25

Sequence: 1 RARY 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mic:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	28.0	6	10 P82181	P82181 spinacia ol
2	7	28.0	6	10 P82182	P82182 spinacia ol
3	6	24.0	6	10 P82541	P82541 spinacia ol
4	5	20.0	5	13 P83308	P83308 gallus gall
5	4	16.0	5	10 Q99007	Q99007 hordeum vul
6	3	12.0	4	11 Q08433	Q08433 rattus norv
7	2	8.0	5	2 P83073	P83073 bacillus ce

ALIGNMENTS

RESULT 1
ID P82181
AC P82181; PRELIMINARY; PRT; 6 AA.

01-JUN-2000 (TREMBlrel. 14, Created)
01-JUN-2000 (TREMBlrel. 14, Last sequence update)
01-MAR-2002 (TREMBlrel. 20, Last annotation update)
Chloroplast 50S ribosomal protein L10 beta (Fragment).
Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
[1]
SEQUENCE.
RC STRAIN=CV. ALWARO; TISSUE=LEAF;
RA MEDLINE=20435798; PubMed=10874046;
RX Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -|- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -|- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -|- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -|- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR001790; Ribosomal_L10.
DR InterPro: IPR002363; Ribosomal_L10eub.
DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
FT SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
Query Match 28.0%; Score 7; DB 10; Length 6;
Best Local Similarity 33.3%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RAR 3
Db 4 RTK 6
RESULT 2
P82182 PRELIMINARY; PRT; 6 AA.
ID P82182
AC P82182;
DT 01-JUN-2000 (TREMBlrel. 14, Created)
DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
[1]
SEQUENCE.
RC STRAIN=CV. ALWARO; TISSUE=LEAF;
RA MEDLINE=20435798; PubMed=10874046;
RX Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -|- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -|- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -|- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -|- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR001790; Ribosomal_L10.
DR InterPro: IPR002363; Ribosomal_L10eub.
DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
FT SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 28.0%; Score 7; DB 10; Length 6;
 Best Local Similarity 33.3%; Pred. No. 6.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAR 3
 | :
 Db 4 RTK 6

RESULT 3
 P82541
 ID P82541 PRELIMINARY; PRT; 6 AA.
 AC P82541;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3362;
 [1]
 RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RP STRAIN=CV. ALVARO; TISSUE=LEAF;
 RC MEDLINE=20435797; PubMed=10874039;
 RX Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RA "The plastid ribosomal proteins. Identification of all the proteins in
 RT the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 37:28455-28465(2000)
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
 CC -1- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
 CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
 CC FORM IS THE MINOR BASIC FORM.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
 CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR002222; Ribosomal_S19.
 DR Pfam: PF00203; Ribosomal_S19; PARTIAL.
 DR PRINTS; PRO0975; RIBOSOMALS19; PARTIAL.
 DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 24.0%; Score 6; DB 10; Length 6;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RA 2
 | :
 Db 2 RS 3

RESULT 4
 P83308
 ID P83308 PRELIMINARY; PRT; 5 AA.
 AC P83308;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE FWRamide-like neuropeptide (LPIRF-amide).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 [1]
 RN SEQUENCE AND SYNTHESIS.
 RP TISSUE=BRAIN;

RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to FWRamide.";
 RL Nature 305:328-330(1983).
 CC -1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FWRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 20.0%; Score 5; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
 | :
 Db 4 R 4

RESULT 5
 Q99007
 ID Q99007 PRELIMINARY; PRT; 5 AA.
 AC Q99007;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE Alpha-amylase (EC 3.2.1.1) (Fragment).
 GN AMY1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellic
 RT acid and abscisic acid in protoplasts prepared from mature barley
 RT aleurone layers.";
 RL Plant Mol. Biol. 16:713-721(1991).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
 CC BARLEY.
 DR EMBL; X54643; CAA38455.1; -;
 KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family.
 FT NON_TER 5
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 16.0%; Score 4; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 A 2
 | :
 Db 2 A 2

RESULT 6
 Q08433
 ID Q08433 PRELIMINARY; PRT; 4 AA.
 AC Q08433;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
 DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT
 DE (Fragment)).
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat."; 177:1161-1164(1991).
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -|- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -|- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -|- SUBCELLULAR LOCATION: MICROSOME.
DR EMBL: S38636; AAB19259.1; -;
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1 1
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 12.0%; Score 3; DB 11; Length 4;
Best Local Similarity 0.0%; Pred. No. 6.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 I 4
DB 2 V 2

RESULT 7
P83073
ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE 88 kDa protein (fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 8.0%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 6.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
DB 2 K 2

Search completed: December 12, 2002, 15:18:46
Job time : 21.25 secs

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:09:28 ; Search time 21.6 Seconds
(without alignments)
24.676 Million cell updates/sec

Title: US-09-600-432-26

Perfect score: 20

Sequence: 1 ARY 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 42205

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002.*

- 1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
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- 19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	4	20	AA198513
2	20	100.0	4	21	AA19068
3	20	100.0	5	20	AA198512
4	20	100.0	5	21	AA19067
5	20	100.0	6	20	AA198511
6	20	100.0	6	21	AA19065
7	19	95.0	6	20	AA19842
8	18	80.0	5	22	AA11144
9	17	85.0	6	17	AAW08720
10	17	85.0	6	17	AAW08721

11	17	85.0	6	17	AAW08722	Trypsin inhibitory
12	17	85.0	6	17	AAW0652	S. acidocaldarius
13	17	85.0	6	19	AAW56944	Enzyme inhibitor p
14	16	80.0	4	10	AAW56944	Motif useful in to
15	16	80.0	4	19	AAW55761	Immunisation motif
16	16	80.0	5	20	AAW55761	Factor xa inhibiti
17	16	80.0	5	21	AAW55761	Claudin-1 cell adh
18	16	80.0	6	21	AAW55761	Claudin-1 cell adh
19	16	80.0	6	21	AAW55761	Claudin-1 cell adh
20	16	80.0	6	21	AAW55761	Claudin-1 cell adh
21	16	80.0	6	23	AAU93629	Granulocyte-colony
22	15	75.0	3	15	AAW61034	ACE-inhibiting tri
23	15	75.0	4	17	AAW5671	Angiotensin II fra
24	15	75.0	4	19	AAW4737	Angiotensin II pep
25	15	75.0	4	19	AAW5606	Angiotensin II ana
26	15	75.0	4	19	AAW71119	Peptide AII(1-4) u
27	15	75.0	4	20	AAW49595	Angiotensin analog
28	15	75.0	4	20	AAW33910	Angiotensin II ana
29	15	75.0	4	20	AAW30548	Angiotensin II ana
30	15	75.0	4	20	AAW30592	Amino acid sequenc
31	15	75.0	4	20	AAW32723	Angiotensin II ana
32	15	75.0	4	20	AAW33777	Angiotensin II (AI
33	15	75.0	4	20	AAW15354	Angiotensin II (AI
34	15	75.0	4	20	AAW15314	Angiotensin II (AI
35	15	75.0	4	21	AAW27410	Angiotensin II ana
36	15	75.0	4	21	AAW28108	Angiotensin II ana
37	15	75.0	4	21	AAW84133	Peptide comprising
38	15	75.0	4	21	AAW59265	Peptide which inhi
39	15	75.0	4	21	AAW77046	Angiotensin II (AI
40	15	75.0	4	21	AAW57410	Angiotensin peptid
41	15	75.0	4	22	AAE08880	AII peptide (resid
42	15	75.0	4	22	AAE02997	Human angiotensin
43	15	75.0	4	22	AAE03160	Human angiotensin
44	15	75.0	4	22	AAW91467	Angiotensin peptid
45	15	75.0	4	23	AAE19194	Angiotensin II pep

ALIGNMENTS

RESULT 1
AAW28513
ID AAW28513 standard; peptide; 4 AA.
XX
AC AAW28513;
XX
DT 19-OCT-1999 (first entry)
XX
DE Beta-1 integrin cell adhesion modulator analogue #26.
XX
KW Beta 1 integrin dependent cell adhesion; Lipar motif; tumour;
KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
XX
OS Synthetic.
XX
PN W09937669-A1.
XX
PD 29-JUL-1999.
XX
PF 21-JAN-1999; 99WO-US01236.
XX
PR 12-AUG-1998; 98US-0096212.
PR 22-JAN-1998; 98US-0072119.
PR 12-AUG-1998; 98US-0096211.
(MINU) UNIV MINNESOTA.
PI Brienza A, Furcht LT, McCarthy JB;
XX
DR WPI, 1999-469112/39.
XX
PT New peptides modulating betal integrin subunit dependent cell
adhesion, useful to study cell adhesion e.g. alpha4beta1 integrin

PT dependent adhesion important in tumour cell biology
 XX Claim 6; Fig 8; 47pp; English.
 PS This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAY28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which
 CC has a side chain including an aromatic group, and a penultimate
 CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
 CC a 'LipAr' motif. Studies with these peptides have also shown that
 CC inhibiting peptides do not contain D-amino acids and that it is the
 CC presence of the ArLip motif that conveys effective beta1 integrin
 CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
 CC cell adhesion is important for cell adhesion to extracellular matrix
 CC proteins, and the subunit is expressed on tumours such as melanomas.
 CC Therefore these LipAr motif containing peptides may be important in the
 CC treatment of cancer.
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARIY 4
 ||||
 Db 1 ARIY 4
 RESULT 2
 AAB19068
 ID AAB19068 standard; peptide; 4 AA.
 XX
 AC AAB19068;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of a beta1-integrin inhibitor.
 XX
 KW Beta1-integrin inhibitor; leukocyte mediated tissue destruction;
 KW central nervous system ischemic injury; myocardial infarction;
 KW beta1-integrin; angioplasty; surgical incision; injury-related trauma;
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX
 OS Synthetic.
 XX
 PN WO2000056350-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US07680.
 XX
 PR 22-MAR-1999; 99US-0125634.
 PR 24-NOV-1999; 99US-0167538.
 XX
 PA (MINU) UNIV MINNESOTA.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (SENT-) SENTRON MEDICAL INC.
 XX
 PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
 PI Furcht LT;
 XX
 DR WPI; 2000-656062/63.
 XX
 PT Inhibition of inflammatory leukocyte mediated destruction of tissue in
 XX a patient, comprises administering a peptide inhibitor of
 PT beta1-integrin, useful for treatment of e.g. cancer and osteoporosis -
 XX
 PS Claim 3; Page 38; 61pp; English.
 XX
 XX AAB19054-67 represent beta1-integrin inhibitors. The peptides inhibit
 CC beta1-integrin which is responsible for leukocyte mediated tissue

CC destruction. The peptides are useful for inhibiting inflammatory
 CC leukocyte mediated destruction of tissue which occurs as a result of
 CC central nervous system (CNS) ischemic injury, myocardial infarction,
 CC angioplasty, surgical incisions, injury-related trauma, and/or
 CC transplant reperfusion, exposure to heat, cold, light, electricity
 CC and/or chemicals. They are also useful for the treatment of stroke, a
 CC burn type injury, cancer, and osteoporosis.
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 20; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARIY 4
 ||||
 Db 1 ARIY 4
 RESULT 3
 AAY28512
 ID AAY28512 standard; peptide; 5 AA.
 XX
 AC AAY28512;
 XX
 DT 19-OCT-1999 (first entry)
 XX
 DE Beta-1 integrin cell adhesion modulator analogue #25.
 XX
 KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX
 OS Synthetic.
 XX
 PN WO9937669-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 21-JAN-1999; 99WO-US01236.
 XX
 PR 12-AUG-1998; 98US-0096212.
 PR 22-JAN-1998; 98US-0072119.
 PR 12-AUG-1998; 98US-0096211.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Brienza A, Furcht LT, McCarthy JB;
 XX
 DR WPI; 1999-469112/39.
 XX
 PT New peptides modulating beta1 integrin subunit dependent cell
 PT adhesion, useful to study cell adhesion e.g. alpha4beta1 integrin
 PT dependent adhesion important in tumour cell biology
 XX
 PS Claim 6; Fig 7; 47pp; English.
 XX
 CC This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAY28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which
 CC has a side chain including an aromatic group, and a penultimate
 CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
 CC a 'LipAr' motif. Studies with these peptides have also shown that
 CC inhibiting peptides do not contain D-amino acids and that it is the
 CC presence of the ArLip motif that conveys effective beta1 integrin
 CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
 CC cell adhesion is important for cell adhesion to extracellular matrix
 CC proteins, and the subunit is expressed on tumours such as melanomas.
 CC Therefore these LipAr motif containing peptides may be important in the
 CC treatment of cancer.
 XX
 SQ Sequence 5 AA;


```

Query Match      100.0%; Score 20; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARIY 4
   ||||
Db 2 ARIY 5

RESULT 4
AAB19067
ID AAB19067 standard; peptide; 5 AA.
XX AC AAB19067;
XX DT 08-FEB-2001 (first entry)
XX DE Amino acid sequence of a betal-integrin inhibitor.
XX KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
XX KW central nervous system ischemic injury; myocardial infarction;
XX KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
XX KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
XX OS Synthetic.
XX PA (MINU ) UNIV MINNESOTA.
XX PN WO200056350-A2.
XX PD 28-SEP-2000.
XX PF 22-MAR-2000; 2000WO-US07680.
XX PR 22-MAR-1999; 99US-0125634.
XX PR 24-NOV-1999; 99US-0167538.
XX PA (MINU ) UNIV MINNESOTA.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PA (SENT-) SENTRON MEDICAL INC.
XX PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
XX PI Furcht LT;
XX DR WPI; 2000-656062/63.
XX CC Inhibition of inflammatory leukocyte mediated destruction of tissue in
XX CC a patient, comprises administering a peptide inhibitor of
XX CC betal-integrin, useful for treatment of e.g. cancer and osteoporosis
XX PS Claim 3; Page 38; 61pp; English.
XX CC AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
XX CC betal-integrin which is responsible for leukocyte mediated tissue
XX CC destruction. The peptides are useful for inhibiting inflammatory
XX CC leukocyte mediated destruction of tissue which occurs as a result of
XX CC central nervous system (CNS) ischemic injury, myocardial infarction,
XX CC angioplasty, surgical incisions, injury-related trauma, and/or
XX CC transplant reperfusion, exposure to heat, cold, light, electricity
XX CC and/or chemicals. They are also useful for the treatment of stroke, a
XX CC burn type injury, cancer, and osteoporosis.
XX SQ Sequence 5 AA;

Query Match      100.0%; Score 20; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARIY 4
   ||||
Db 2 ARIY 5

RESULT 5
AAB28511
ID AAB19067 standard; peptide; 5 AA.
XX AC AAB19067;
XX DT 08-FEB-2001 (first entry)
XX DE Amino acid sequence of a betal-integrin inhibitor.
XX KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
XX KW central nervous system ischemic injury; myocardial infarction;
XX KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
XX KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
XX OS Synthetic.
XX PA (MINU ) UNIV MINNESOTA.
XX PN WO200056350-A2.
XX PD 28-SEP-2000.
XX PF 22-MAR-2000; 2000WO-US07680.
XX PR 22-MAR-1999; 99US-0125634.
XX PR 24-NOV-1999; 99US-0167538.
XX PA (MINU ) UNIV MINNESOTA.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PA (SENT-) SENTRON MEDICAL INC.
XX PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
XX PI Furcht LT;
XX DR WPI; 2000-656062/63.
XX CC Inhibition of inflammatory leukocyte mediated destruction of tissue in
XX CC a patient, comprises administering a peptide inhibitor of
XX CC betal-integrin, useful for treatment of e.g. cancer and osteoporosis
XX PS Claim 3; Page 38; 61pp; English.
XX CC AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
XX CC betal-integrin which is responsible for leukocyte mediated tissue
XX CC destruction. The peptides are useful for inhibiting inflammatory
XX CC leukocyte mediated destruction of tissue which occurs as a result of
XX CC central nervous system (CNS) ischemic injury, myocardial infarction,
XX CC angioplasty, surgical incisions, injury-related trauma, and/or
XX CC transplant reperfusion, exposure to heat, cold, light, electricity
XX CC and/or chemicals. They are also useful for the treatment of stroke, a
XX CC burn type injury, cancer, and osteoporosis.
XX SQ Sequence 5 AA;

Query Match      100.0%; Score 20; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARIY 4
   ||||
Db 3 ARIY 6

RESULT 6
AAB19065
ID AAB19065 standard; peptide; 6 AA.
XX AC AAB19065;
XX DT 08-FEB-2001 (first entry)
XX DE Amino acid sequence of a betal-integrin inhibitor.
XX KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
XX KW central nervous system ischemic injury; myocardial infarction;

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ID AAV28511 standard; peptide; 6 AA.
XX AC AAV28511;
XX DT 19-OCT-1999 (first entry)
XX DE Beta-1 integrin cell adhesion modulator analogue #24.
XX KW Beta 1 integrin dependent cell adhesion; LipAR motif; tumour;
XX KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
XX OS Synthetic.
XX PN WO9937669-A1.
XX PD 29-JUL-1999.
XX PF 21-JAN-1999; 99WO-US01236.
XX PR 12-AUG-1998; 98US-0096212.
XX PR 22-JAN-1998; 98US-0072119.
XX PR 12-AUG-1998; 98US-0096211.
XX PA (MINU ) UNIV MINNESOTA.
XX PI Brienza A, Furcht LT, McCarthy JB;
XX DR WPI; 1999-469112/39.
XX PT New peptides modulating betal integrin subunit dependent cell
XX PT adhesion, useful to study cell adhesion e.g. alpha4betal integrin
XX PS dependent adhesion important in tumour cell biology
XX PS Claim 6; Fig 7; 47pp; English.
XX CC This sequence is a C-terminal tyrosine tagged peptide. This peptide
XX CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
XX CC AAV28510-Y28549 have been used to show that peptides which modulate this
XX CC form of cell adhesion need a C-terminal amino acid residue (Ar) which
XX CC has a side chain including an aromatic group, and a penultimate
XX CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
XX CC a 'LipAr' motif. Studies with these peptides have also shown that
XX CC inhibiting peptides do not contain D-amino acids and that it is the
XX CC presence of the ArLip motif that conveys effective betal integrin
XX CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
XX CC cell adhesion is important for cell adhesion to extracellular matrix
XX CC proteins, and the subunit is expressed on tumours such as melanomas.
XX CC Therefore these LipAr motif containing peptides may be important in the
XX CC treatment of cancer.
XX SQ Sequence 6 AA;

Query Match      100.0%; Score 20; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARIY 4
   ||||
Db 3 ARIY 6

RESULT 6
AAB19065
ID AAB19065 standard; peptide; 6 AA.
XX AC AAB19065;
XX DT 08-FEB-2001 (first entry)
XX DE Amino acid sequence of a betal-integrin inhibitor.
XX KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
XX KW central nervous system ischemic injury; myocardial infarction;

```



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XX OS Unidentified.
XX PN W0200168822-A2.
XX XX 20-SEP-2001.
XX PF 14-MAR-2001; 2001WO-DK00172.
XX PR 14-MAR-2000; 2000US-0525116.
XX PA (NILA-) NILAB APS.
XX PI Johnsen M, Ravn P, Madsen SM, Vrang A, Israelsen H, Bredmose L;
XX PI Arnau J, Jensen SH, Gjetting T, Nielsen E;
XX PR WPI; 2001-590055/66.
XX DR Novel recombinant cells comprising a nucleic acid encoding a gene
XX PT product having phenylalanine hydroxylase activity, that is derived from
XX PT a prokaryotic organism, is useful for treating phenylketonuria in
XX PT mammals.
XX PS Example 8; Page 48; 91pp; English.
XX CC The patent discloses novel cells comprising a nucleic acid encoding
XX CC a gene product having phenylalanine hydroxylase (PAH) activity such
XX CC as phenylalanine hydroxylase (phhA), 4a-carbinolamine dehydratase
XX CC (phhB) and aromatic aminotransferase (phhC), which are derived
XX CC from a prokaryotic organism. The patent also relates to fusion
XX CC proteins comprising a protein enhancing and/or stabilising the
XX CC PAH activity in addition to PAH activity. The cells are useful
XX CC for producing PAH. The sequences of the invention are also useful
XX CC for preparing a proteinaceous food product (animal protein such
XX CC as a milk protein derived from casein, globulin or a whey protein)
XX CC having reduced content of phenylalanine. The method involves contacting
XX CC the food product starting material with the cells or fusion proteins
XX CC such that at least part of the phenylalanine content of the starting
XX CC material is converted into compounds that do not cause phenylketonuria
XX CC (PKU) by the enzymatically active product. PAH enzyme is useful for
XX CC manufacturing a medicament for treating PKU, which is an inherited
XX CC metabolic disorder resulting in an accumulation in the body of
XX CC L-phenylalanine and metabolites that can cause impaired brain
XX CC function. The present sequence is chymotryptic peptide of phhAB fusion
XX CC protein.
XX SQ Sequence 5 AA;
XX
XX Query Match 90.0%; Score 18; DB 22; Length 5;
XX Best Local Similarity 75.0%; Pred. No. 7.8e+05;
XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ARIY 4
XX DB 2 ARLY 5
XX
XX RESULT 9
XX AAW08720
XX ID AAW08720 standard; peptide; 6 AA.
XX AC AAW08720;
XX XX 28-FEB-1997 (first entry)
XX DT Trypsin inhibitory peptide #1.
XX DE Ligand; synthetic combinatorial peptide library; hexamer; antibody;
XX KW antigen; receptor; inhibitor; trypsin.
XX XX Synthetic.
XX OS Key Location/Qualifiers
XX FH Modified-site 1
XX FT /label= "Ac-Ala"
XX FT /note= "Ac-Ala"

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FT Modified-site 1
FT /label= OTHER
FT /note= "Ac-Ala"
FT Modified-site 6
FT /label= OTHER
FT /note= "Pro-NH2"
XX US5556762-A.
XX PN 17-SEP-1996.
XX PD 21-NOV-1990; 90US-0617023.
XX PF 11-SEP-1992; 92US-0943709.
XX PR 21-NOV-1990; 90US-0617023.
XX PR 16-MAY-1991; 91US-0701658.
XX PR 19-NOV-1991; 91US-0797551.
XX PA (HOUG-) HOUGHTEN PHARM INC.
XX PI Appel JR, Houghten RA, Pinilla C;
XX DR WPI; 1996-432985/43.
XX PS Identifying oligopeptide ligands for an acceptor - by scanning
XX PT synthetic peptide combinatorial libraries comprising
XX PT self-solubilising, unsupported mixed oligopeptide(s)
XX XX Example 8; Column 59; 75pp; English.
XX CC The invention relates to a method of identifying oligopeptide ligands to
XX CC a protein by scanning synthetic combinatorial peptide libraries (SCPL).
XX CC The SCPL comprise sets of hexamers which contain either one of 6
XX CC predetermined amino acids at one predetermined position in the hexamer
XX CC and each set may have one predetermined amino acid at 1 of 6
XX CC predetermined pos. in the hexamer. The method is useful for identifying
XX CC biologically active sequences of e.g. pharmaceutical use. The peptides
XX CC esp. inhibit the binding of e.g. an antibody to its antigen, a ligand to
XX CC its receptor, etc.
XX CC The peptides AAW08720-25 are N-terminally acylated and C-terminally
XX CC amidated peptides, isolated from a SCPL, which inhibit trypsin.
XX CC This peptide inhibited trypsin with an IC50 of 46 micromole.
XX SQ Sequence 6 AA;
XX
XX Query Match 85.0%; Score 17; DB 17; Length 6;
XX Best Local Similarity 75.0%; Pred. No. 7.8e+05;
XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ARIY 4
XX DB 1 AKIY 4
XX
XX RESULT 10
XX AAW08721
XX ID AAW08721 standard; peptide; 6 AA.
XX AC AAW08721;
XX XX 28-FEB-1997 (first entry)
XX DT Trypsin inhibitory peptide #2.
XX DE Ligand; synthetic combinatorial peptide library; hexamer; antibody;
XX KW antigen; receptor; inhibitor; trypsin.
XX XX Synthetic.
XX OS Key Location/Qualifiers
XX FH Modified-site 1
XX FT /label= "Ac-Ala"
XX FT /note= "Ac-Ala"

```


PR 21-NOV-1994; 94JP-0286917.
 PR 21-NOV-1994; 94JP-0311185.
 XX (KIRI) KIRIN BEER KK.
 XX WPI; 1996-049671/05.
 XX Sulfolobus spp. derived transferase and amylase - for production of
 PT alpha, alpha-trehalose from malto-oligosaccharide(s)
 XX Example I-11; Page 179; 357pp; Japanese.
 XX AAR90652-54 are Asp-N peptide fragments of a transferase isolated from
 CC Sulfolobus acidocaldarius. The transferase (AAR90618) acts on a
 CC saccharide having at least three sugar units, in which at least three
 CC glucose units at the reducing end are alpha-1,4 linked, to transform the
 CC alpha-1,4 linkages to alpha-1, linkages. The transferase has a
 CC mol. wt. of 74 to 76 kDa. It is characterised by working at pH 4.5-6.0
 CC and at 60-80 deg.C. It has an isoelectric point of 5.3-6.3 and retains
 CC at least 90 percent activity after 6 hrs. at 80 deg.C. It is completely
 CC inhibited by 5 mM copper sulphate. Use of the transferase and an amylase
 CC in succession on suitable substrates such as malto-oligosaccharides, is
 CC useful for the production of alpha, alpha-trehalose.
 XX SQ Sequence 6 AA;
 Query Match 85.0%; Score 17; DB 17; Length 6;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARIY 4
 Db :|||
 3 SRIY 6
 RESULT 13
 ID AAW56944 standard; peptide; 6 AA.
 XX AC AAW56944;
 XX 28-JUL-1998 (first entry)
 DE Enzyme inhibitor peptide SEQ ID NO:145.
 DE Enzyme inhibitor; t-PA; u-PA; chymotrypsin; serine protease; active;
 KW latent; substrate subtraction phage display peptide library;
 KW identification; kinase; phosphatase; serpin.
 XX OS Homo sapiens.
 XX WO9747314-A1.
 XX 18-DEC-1997.
 XX 10-JUN-1997; 97WO-US09760.
 XX 10-JUN-1996; 96US-0019495.
 XX (SCRI) SCRIPPS RES INST.
 XX Ke S, Madison EL;
 XX WPI; 1998-062746/06.
 XX Substrate subtraction phage display peptide libraries - used to
 PT distinguish between active and latent forms of enzyme, e.g. serine
 PT protease
 XX Claim 25; Page 89; 138pp; English.
 XX The present sequence represents an enzyme inhibitor peptide used in
 CC the method of the invention to distinguish between t-PA and u-PA. The

CC present invention describes a substrate subtraction library for the
 CC identification of peptide substrates selective between a first enzyme
 CC (E1) and a second enzyme (E2), comprising a collection different
 CC peptides, substantially lacking peptides that are effective substrates
 CC for E1. Also described are: (1) a method (M1) for identifying peptide
 CC substrates selective between a first enzyme (E1) and a second enzyme
 CC (E2); (2) a compound comprising the amino acid sequence of a peptide
 CC identified by M1; (3) a polypeptide for use as an enzyme inhibitor
 CC comprising one of 237 amino acid sequences (see AAW56801 to AAW56947,
 CC and AAW56949 to AAW57038); (4) a recombinant DNA vector comprising DNA
 CC (1) encoding a protease inhibitor including the sequence identified by
 CC the M1; (5) a prokaryotic or eukaryotic cell containing the vector of
 CC (4); (6) an antibody (Ab) immunoreactive with at least one of the
 CC peptides identified by M1; and (7) a diagnostic assay for distinguishing
 CC between active and latent forms of protease inhibitors, that uses (Ab).
 CC The library and method are used for distinguishing between active and
 CC latent forms of enzyme inhibitors, e.g. proteases, kinases and
 CC phosphatases. (Ab) are used for affinity purification of recombinant
 CC peptides and in the identification of naturally occurring protease
 CC inhibitors. Enzyme-inhibiting peptides identified can be used to treat a
 CC serpin deficiency or a disorder of serine proteases.
 XX SQ Sequence 6 AA;
 Query Match 85.0%; Score 17; DB 19; Length 6;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARIY 4
 Db :|||
 2 ARMY 5
 RESULT 14
 AAR91620
 ID AAP91620 standard; protein; 4 AA.
 XX AC AAP91620;
 XX 09-JUL-1990 (first entry)
 DE Motif useful in tolerization alone or in association with epitopes to
 DE peripheral nervous system myelin protein, a proteolipid protein, a PNS and
 DE CNS myelin constituent and the acetyl choline receptor.
 XX Autoantigen; MBP; myelin basic protein; transplantation antigen;
 KW myasthenia gravis; myasthenics; Transplantation antigen.
 XX Synthetic.
 XX EP304279-A.
 XX 22-FEB-1989.
 XX 17-AUG-1988; 88EP-0307608.
 XX 17-AUG-1988; 88US-0086694.
 XX (STRD) LELAND STANFORD JR UNIV.
 XX Steinman L;
 XX WPI; 1989-055696/08.
 XX Oligopeptide and polypeptide compsns. -
 PT based on the amino acid sequence of an immunogen and used for
 PT modulating the immune system.
 XX Disclosure; ; 7pp; English.
 XX Sequences will normally be part of 9-15 amino acid sequence, excluded as
 CC motifs for immunisation but useful in tolerisation..
 XX

```

SQ Sequence 4 AA;
  Query Match      80.0%; Score 16; DB 10; Length 4;
  Best Local Similarity 100.0%; Pred. No. 7.8e+05;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIY 4
   |||
Db 1 RIY 3

RESULT 15
AAW55761
ID AAW55761 standard; peptide; 4 AA.
XX
AC AAW55761;
XX
XX 08-JUL-1998 (first entry)
XX Immunisation motif associated with P2 8.
XX
XX Myelin basic protein; immunity; immune response; neurological; T-cell;
KW human; immunogen; B-cell; transplantation antigen; immunomodulator.
XX
XX Unidentified.
XX
XX EP805162-A1.
XX
XX 05-NOV-1997.
XX
XX PF 17-AUG-1988; 88EP-0307608.
XX
XX PR 17-AUG-1987; 87US-0086694.
XX
XX (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
XX Steinman L, Zamvil S;
XX
XX WPI; 1998-034664/04.
XX
XX Polypeptide comprising human myelin basic protein fragment - useful
PT as immuno modulator
XX
XX Disclosure; Page 8; 8pp; English.
XX
XX The present sequence represents an immunisation motif normally excluded,
CC but which may be used with advantage for tolerisation by itself or in
CC conjunction with other epitope sequences from the present invention. The
CC present invention describes a polypeptide comprising a human myelin basic
CC protein (hMBP) fragment including P89-101 of hMBP, excluding native hMBP.
CC The term P89-101 is not defined but may be intended to mean amino acids
CC 89-101 of hMBP. The polypeptide can be used for tolerising a mammalian
CC host immune system comprising B and T cells to an immunogen of interest,
CC wherein said immunogen is restricted by a transplantation antigen of said
CC host.
XX
SQ Sequence 4 AA;
  Query Match      80.0%; Score 16; DB 19; Length 4;
  Best Local Similarity 100.0%; Pred. No. 7.8e+05;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIY 4
   |||
Db 1 RIY 3

Search completed: December 12, 2002, 15:17:16
Job time : 22.6 secs

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OW protein - protein search, using sw model

Run on: December 12, 2002, 15:15:23 ; Search time 7.6 Seconds
(without alignments)

15.486 Million cell updates/sec

Title: US-09-600-432-26

Perfect score: 20

Sequence: 1 ARY 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: ~ 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 32749

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	15	75.0	4	2	US-08-465-775-10
2	15	75.0	4	3	US-09-208-337-10
3	15	75.0	4	3	US-08-990-664-11
4	15	75.0	4	4	US-09-373-962-10
5	15	75.0	4	4	US-09-245-680-10
6	15	75.0	4	4	US-09-198-806C-10
7	15	75.0	4	4	US-09-352-191-10
8	15	75.0	4	4	US-09-012-400-10
9	15	75.0	4	4	US-09-264-563-10
10	15	75.0	5	2	US-08-465-775-9
11	15	75.0	5	3	US-08-812-586-58
12	15	75.0	5	3	US-09-208-337-9
13	15	75.0	5	3	US-08-990-664-10
14	15	75.0	5	4	US-09-373-962-9
15	15	75.0	5	4	US-09-245-680-9
16	15	75.0	5	4	US-09-198-806C-9
17	15	75.0	5	4	US-09-352-191-9
18	15	75.0	5	4	US-09-012-400-9
19	15	75.0	5	4	US-09-264-563-9
20	15	75.0	6	2	US-08-623-833B-26
21	15	75.0	6	2	US-08-465-775-5
22	15	75.0	6	3	US-09-208-337-5
23	15	75.0	6	3	US-08-990-664-5
24	15	75.0	6	3	US-09-208-337-8
25	15	75.0	6	3	US-08-990-664-6
26	15	75.0	6	3	US-08-990-664-9
27	15	75.0	6	4	US-09-373-962-5

28 15 75.0 6 4 US-09-373-962-8 Sequence 8, Appli
29 15 75.0 6 4 US-09-117-339-6 Sequence 6, Appli
30 15 75.0 6 4 US-09-245-680-5 Sequence 5, Appli
31 15 75.0 6 4 US-09-245-680-8 Sequence 8, Appli
32 15 75.0 6 4 US-09-198-806C-5 Sequence 5, Appli
33 15 75.0 6 4 US-09-198-806C-8 Sequence 8, Appli
34 15 75.0 6 4 US-09-352-191-5 Sequence 5, Appli
35 15 75.0 6 4 US-09-352-191-8 Sequence 8, Appli
36 15 75.0 6 4 US-09-012-400-5 Sequence 5, Appli
37 15 75.0 6 4 US-09-012-400-8 Sequence 8, Appli
38 15 75.0 6 4 US-09-264-563-5 Sequence 5, Appli
39 15 75.0 6 4 US-09-264-563-8 Sequence 8, Appli
40 14 70.0 6 6 5208144-9 Patent No. 5208144
41 13 65.0 4 1 US-08-079-812-50 Sequence 50, Appl
42 13 65.0 4 2 US-08-480-133A-15 Sequence 15, Appl
43 13 65.0 4 3 US-09-008-308-30 Sequence 30, Appl
44 13 65.0 4 3 US-09-008-308-32 Sequence 32, Appl
45 13 65.0 4 3 US-09-020-299-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-465-775-10
; Sequence 10, Application US/08465775
; Patent No. 5955430
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen E.
; APPLICANT: Gizegaga, Gere S.
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Robbins, Berliner & Carson
; STREET: 201 No. 5955430th Figueroa Street #500
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,775
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 1920-360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-775-10

Query Match 75.0%; Score 15; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4

DB 2 RY 4

RESULT 2
US-09-208-337-10
; Sequence 10, Application US/09208337
; Patent No. 6096709
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: Gerez, Gerez
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS
; TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,337
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,775
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: 08/337,781
; FILING DATE: 14-NOV-1994
; APPLICATION NUMBER: 08/126,368
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC010.001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 949-760-0404
; TELEFAX: 949-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-208-337-10
Query Match 75.0%; Score 15; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 RY 4
DB 2 RV 4
RESULT 3
US-08-990-664-11
; Sequence 11, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: Gerez, Gerez
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING
; TITLE OF INVENTION: IN SKIN GRAFTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach

; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,664
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028,310
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC012.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-990-664-11
Query Match 75.0%; Score 15; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 RY 4
DB 2 RV 4
RESULT 4
US-09-373-962-10
; Sequence 10, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: Gerez, Gerez
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
; FILE REFERENCE: 98364A
; CURRENT APPLICATION NUMBER: US/09/373,962
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-373-962-10
Query Match 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 RY 4
DB 2 RV 4
RESULT 5
US-09-245-680-10

; Sequence 10, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method of Promoting Erythropoiesis
; FILE REFERENCE: 98009B
; CURRENT APPLICATION NUMBER: US/09/245,680B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-245-680-10

Query Match 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYI 4
;:
Db 2 RVI 4

RESULT 6
US-09-198-806C-10
; Sequence 10, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation
; FILE REFERENCE: 97,017-F1
; CURRENT APPLICATION NUMBER: US/09/198,806C
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-198-806C-10

Query Match 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYI 4
;:
Db 2 RVI 4

RESULT 7
US-09-352-191-10
; Sequence 10, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
; TITLE OF INVENTION: Growth and Repair
; FILE REFERENCE: 98365B
; CURRENT APPLICATION NUMBER: US/09/352,191
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-352-191-10

Query Match 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYI 4
;:
Db 2 RVI 4

RESULT 8
US-09-012-400-10
; Sequence 10, Application US/09012400D
; Patent No. 6335195
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
; TITLE OF INVENTION: Proliferation and Differentiation
; FILE REFERENCE: 97,017-G
; CURRENT APPLICATION NUMBER: US/09/012,400D
; CURRENT FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-012-400-10

Query Match 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYI 4
;:
Db 2 RVI 4

RESULT 9
US-09-264-563-10
; Sequence 10, Application US/09264563A
; Patent No. 6455500
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017K1
; CURRENT APPLICATION NUMBER: US/09/264,563A
; CURRENT FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-264-563-10

Query Match 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIV 4
1:1
DB 2 RIV 4

RESULT 10

US-08-465-775-9
; Sequence 9, Application US/08465775
; Patent No. 5955430
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen E.
; APPLICANT: dzerega, Gere S.
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Robbins, Berliner & Carson
; STREET: 201 No. 5955430th Figueroa Street #500
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08465,775
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 1920-360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-775-9

Query Match 75.0%; Score 15; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIV 4
1:1
DB 2 RIV 4

RESULT 11

US-08-812-586-58
; Sequence 58, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-58

Query Match 75.0%; Score 15; DB 3; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIV 4
1:1
DB 1 RIV 3

RESULT 12

US-09-208-337-9
; Sequence 9, Application US/09208337
; Patent No. 6096709
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: Gere, dzerega
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS
; TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,337
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,775
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: 08/337,781
; FILING DATE: 14-NOV-1994
; APPLICATION NUMBER: 08/126,368
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC010.001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 949-760-0404
; TELEFAX: 949-760-9502

TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-208-337-9

Query Match 75.0%; Score 15; DB 3; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
|:|
DB 2 RY 4

RESULT 13
US-08-990-664-10
; Sequence 10, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzizerega, Gere
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING
; TITLE OF INVENTION: IN SKIN GRAFTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,664
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028,310
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC012.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-990-664-10

Query Match 75.0%; Score 15; DB 3; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
|:|
DB 2 RY 4

RESULT 14
US-09-373-962-9
; Sequence 9, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzizerega, Gere
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
; FILE REFERENCE: 98364A
; CURRENT APPLICATION NUMBER: US/09/373,962
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)
US-09-373-962-9

Query Match 75.0%; Score 15; DB 4; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
|:|
DB 2 RY 4

RESULT 15
US-09-245-680-9
; Sequence 9, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzizerega, Gere
; TITLE OF INVENTION: Method of Promoting Erythropoiesis
; FILE REFERENCE: 98009B
; CURRENT APPLICATION NUMBER: US/09/245,680B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)
US-09-245-680-9

Query Match 75.0%; Score 15; DB 4; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
|:|
DB 2 RY 4

Search completed: December 12, 2002, 15:20:54
JOB time : 8.6 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:17:24 ; Search time 4.2 Seconds
(without alignments)
15.869 Million cell updates/sec

Title: US-09-600-432-26
Perfect score: 20
Sequence: 1 ARIV 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105981 seqs, 16662342 residues

Total number of hits satisfying chosen parameters: 5573

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	80.0	4	8	US-08-484-409-24
2	15	75.0	4	9	US-09-900-936-10
3	15	75.0	4	10	US-09-771-192-10
4	15	75.0	4	10	US-09-837-697A-10
5	15	75.0	5	9	US-09-900-936-9
6	15	75.0	5	10	US-09-771-192-9
7	15	75.0	5	10	US-09-837-697A-9
8	15	75.0	6	9	US-09-900-936-5
9	15	75.0	6	9	US-09-900-936-8
10	15	75.0	6	10	US-09-771-192-5
11	15	75.0	6	10	US-09-771-192-8
12	15	75.0	6	10	US-09-837-697A-5
13	15	75.0	6	10	US-09-837-697A-8
14	13	65.0	4	8	US-08-484-409-31
15	13	65.0	4	10	US-09-010-714-10
16	13	65.0	4	12	US-10-041-030-25
17	13	65.0	5	10	US-09-748-114-28
18	12	60.0	4	10	US-09-947-387-48
19	12	60.0	5	10	US-09-947-387-47

20	12	60.0	5	10	US-09-947-387-92	Sequence 92, Appl
21	12	60.0	5	10	US-09-947-387-127	Sequence 127, App
22	12	60.0	5	10	US-09-071-838-266	Sequence 266, App
23	12	60.0	6	9	US-09-981-876-277	Sequence 277, App
24	12	60.0	6	9	US-10-024-918-7	Sequence 7, Appl
25	12	60.0	6	9	US-09-813-718-44	Sequence 44, Appl
26	12	60.0	6	10	US-09-887-469-20	Sequence 20, Appl
27	12	60.0	6	10	US-09-947-387-91	Sequence 91, Appl
28	12	60.0	6	10	US-09-947-387-118	Sequence 62, Appl
29	12	60.0	6	10	US-09-911-838-62	Sequence 118, App
30	12	60.0	6	10	US-09-911-838-64	Sequence 62, Appl
31	12	60.0	6	10	US-09-911-838-66	Sequence 64, Appl
32	12	60.0	6	12	US-10-156-820-45	Sequence 66, Appl
33	12	60.0	6	12	US-10-156-820-76	Sequence 45, Appl
34	11	55.0	4	9	US-09-264-516A-19	Sequence 76, Appl
35	11	55.0	4	9	US-09-769-145-58	Sequence 19, Appl
36	11	55.0	4	10	US-09-731-242A-2	Sequence 58, Appl
37	11	55.0	4	10	US-09-569-193A-18	Sequence 2, Appl
38	11	55.0	4	10	US-09-071-838-240	Sequence 18, Appl
39	11	55.0	5	9	US-10-014-485A-63	Sequence 240, App
40	11	55.0	5	9	US-10-014-485A-67	Sequence 63, Appl
41	11	55.0	5	9	US-10-014-485A-73	Sequence 67, Appl
42	11	55.0	5	10	US-09-813-653-8	Sequence 73, Appl
43	11	55.0	5	10	US-09-217-268B-32	Sequence 8, Appl
44	11	55.0	5	10	US-09-982-172-76	Sequence 32, Appl
45	11	55.0	5	10	US-09-813-448-5	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-08-484-409-24
; Sequence 24, Application US/08484409
; Patent No. US20020076412A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Zamvil, Scott
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,409
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.409C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-484-409-24

Query Match 80.0%; Score 16; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYI 4
| | |
Db 1 RYI 3

RESULT 2

US-09-900-936-10
; Sequence 10, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 97,017-F1A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-900-936-10

Query Match 75.0%; Score 15; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYI 4
| | |
Db 2 RYI 4

RESULT 3

US-09-771-192-10
; Sequence 10, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-771-192-10

Query Match 75.0%; Score 15; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYI 4
| | |
Db 2 RYI 4

RESULT 4

US-09-837-697A-10
; Sequence 10, Application US/09837697A
; Patent No. US20020146823A1
; GENERAL INFORMATION:

; APPLICANT: University of Southern California
; APPLICANT: Rodgers, Kathleen E.
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
; FILE REFERENCE: 97,017-F1A
; CURRENT APPLICATION NUMBER: US/09/837,697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: AII(1-4)
US-09-837-697A-10

Query Match 75.0%; Score 15; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYI 4
| | |
Db 2 RYI 4

RESULT 5

US-09-900-936-9
; Sequence 9, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)
US-09-900-936-9

Query Match 75.0%; Score 15; DB 9; Length 5;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYI 4
| | |
Db 2 RYI 4

RESULT 6

US-09-771-192-9
; Sequence 9, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
US-09-771-192-9

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)
US-09-771-192-9

Query Match      75.0%; Score 15; DB 10; Length 5;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
   | |
Db 2 RY 4

RESULT 7
US-09-837-697A-9
; Sequence 9, Application US/09837697A
; Patent No. US20020146823A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rodgers, Kathleen E.
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
; TITLE OF INVENTION: Differentiation
; FILE REFERENCE: 97,017-FlA
; CURRENT APPLICATION NUMBER: US/09/837,697A
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: AII(1-5)
US-09-837-697A-9

Query Match      75.0%; Score 15; DB 10; Length 5;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
   | |
Db 2 RY 4

RESULT 8
US-09-900-936-5
; Sequence 5, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; TITLE OF INVENTION: or Differentiation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (2-7)
US-09-900-936-5

Query Match      75.0%; Score 15; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 RY 4
   | |
Db 1 RY 3

RESULT 9
US-09-900-936-8
; Sequence 8, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; TITLE OF INVENTION: or Differentiation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)
US-09-900-936-8

Query Match      75.0%; Score 15; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
   | |
Db 2 RY 4

RESULT 10
US-09-771-192-5
; Sequence 5, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (2-7)
US-09-771-192-5

Query Match      75.0%; Score 15; DB 10; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
   | |
Db 1 RY 3

RESULT 11
US-09-771-192-8
; Sequence 8, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere

```

```
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)
US-09-771-192-8

Query Match          75.0%; Score 15; DB 10; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 RY 4
       1:1
Db      2 RY 4

RESULT 12
US-09-837-697A-5
; Sequence 5, Application US/09837697A
; Patent No. US20020146823A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rogers, Kathleen E.
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
; FILE REFERENCE: 97,017-FIA
; CURRENT APPLICATION NUMBER: US/09/837,697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AII(2-7)
US-09-837-697A-5

Query Match          75.0%; Score 15; DB 10; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 RY 4
       1:1
Db      1 RY 3

RESULT 13
US-09-837-697A-8
; Sequence 8, Application US/09837697A
; Patent No. US20020146823A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rogers, Kathleen E.
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
; FILE REFERENCE: 97,017-FIA
; CURRENT APPLICATION NUMBER: US/09/837,697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AII(1-6)
US-09-837-697A-8

Query Match          75.0%; Score 15; DB 10; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 RY 4
       1:1
Db      2 RY 4

RESULT 14
US-08-484-409-31
; Sequence 31, Application US/08484409
; Patent No. US20020076412A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Zamvil, Scott
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,409
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.409C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-484-409-31

Query Match          65.0%; Score 13; DB 8; Length 4;
Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 RY 4
       1:1
Db      1 RY 3

RESULT 15
US-09-010-714-10
; Sequence 10, Application US/09010714
; Patent No. US20020012942A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; APPLICANT: Iida, Joji
; TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
; TITLE OF INVENTION: ACTIVITY
```



```
; FILE REFERENCE: 600.332US01
; CURRENT APPLICATION NUMBER: US/09/010,714
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-010-714-10

Query Match      65.0%; Score 13; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARI 3
        |||
Db       2 ARI 4

Search completed: December 12, 2002, 15:21:21
Job time : 5.2 secs
```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:58 ; Search time 8.8 Seconds
(without alignments)
43.697 Million cell updates/sec

Title: US-09-600-432-26

Perfect score: 20

Sequence: 1 ARI 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	13	65.0	5	2	S62883	seminal plasma pro
2	11	55.0	4	2	PT0721	T-cell receptor be
3	11	55.0	5	3	JT0870	phytosulfofokine alp
4	10	50.0	6	2	JN0861	peptidyl-dipeptida
5	10	50.0	6	2	I49421	laminin B1 - weste
6	9	45.0	4	2	I61883	protamine P1 - ora
7	9	45.0	4	2	I37013	protamine P1 - Cer
8	9	45.0	4	2	I84439	protamine P1 - sav
9	9	45.0	5	2	I40702	primase - Citrobac
10	9	45.0	5	2	I39964	ribosomal protein
11	9	45.0	5	2	I39966	ribosomal protein
12	9	45.0	5	2	I39965	ribosomal protein
13	9	45.0	5	2	P00009	angiotensin-conver
14	9	45.0	6	2	I37027	protamine P1 gor
15	9	45.0	6	2	PT0568	T-cell receptor be
16	7	35.0	3	3	A22565	R-phycoerythrin al
17	7	35.0	3	3	A43391	TdR-like tripeptid
18	7	35.0	3	3	S68328	blood cell protein
19	7	35.0	4	2	A32039	tyrosine-melanocyt
20	7	35.0	4	2	A37832	phenol 2-monooxyge
21	7	35.0	4	2	S09478	globulin IV alpha
22	7	35.0	4	2	PT0240	Ig heavy chain CRD
23	7	35.0	4	2	S43959	Ig mu chain V regi
24	7	35.0	4	2	PT0697	T-cell receptor be
25	7	35.0	5	1	H0R0HA	proctolin - Americ
26	7	35.0	5	2	B37325	pap fibrillar regul
27	7	35.0	5	2	I40469	dnazX-like protein
28	7	35.0	5	2	E60274	major protein anti
29	7	35.0	5	2	F22565	R-phycoerythrin ga

30	7	35.0	5	2	P00689	photosystem I 10.4
31	7	35.0	5	2	B61445	Ieu-enkephalin - b
32	7	35.0	5	2	A61445	Met-enkephalin - b
33	7	35.0	5	2	A60411	proctolin - Atlant
34	7	35.0	5	2	S53595	hypothetical prote
35	7	35.0	5	2	PT0278	Ig heavy chain CRD
36	7	35.0	5	2	S68326	blood cell protein
37	7	35.0	6	2	S02617	alcohol dehydrogen
38	7	35.0	6	2	A61411	ameletin - rat
39	7	35.0	6	2	S11556	hydrogensulfite re
40	7	35.0	6	2	B44510	hypothetical prote
41	7	35.0	6	2	B33932	Ig mu chain D regi
42	7	35.0	6	2	F41946	T-cell receptor ga
43	7	35.0	6	2	A41946	T-cell receptor ga
44	6	30.0	4	2	PL0146	carbon-monoxide de
45	6	30.0	4	2	I40804	endoglucanase F -

ALIGNMENTS

RESULT 1

S62883
seminal plasma protein II - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S62883
R:Romero, A.; Varela, P.F.; Sanz, L.; Toepfer-Petersen, E.; Calvete, J.J.
FEBS Lett. 382, 15-17, 1996
A:Title: Crystallization and preliminary X-ray diffraction analysis of boar seminal p
A:Reference number: S62882; MUID:96196555; PMID:8612739
A:Accession: S62883
A:Molecule type: protein
A:Residues: 1-5 <ROM>
C:Complex: heterodimer; seminal plasma protein I and seminal plasma protein II
C:Keywords: glycoprotein; heterodimer; semen

Query Match 65.08; Score 13; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARI 3
|||
Db 1 ARI 3

RESULT 2

PT0721
T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0721
J:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0721
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 55.0%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARI 3
|||
Db 1 ARI 3

RESULT 3

JT0870
phytosulfokine alpha - garden asparagus (fragment)
C:Species: Asparagus officinalis (garden asparagus)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 19-Apr-2002
C:Accession: JT0870
R:Matsubayashi, Y.; Sakagami, Y.
Proc. Natl. Acad. Sci. U.S.A. 93, 7623-7627, 1996
A:Title: Phytosulfokine, sulfated peptides that induce the proliferation of single mesophyll cells
A:Reference number: JT0870
A:Accession: JT0870
A:Molecule type: protein
A:Residues: 1-5 <MAT>

Query Match 55.0%; Score 11; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IY 4
||
Db 2 IY 3

RESULT 4
JN0861
peptidyl-dipeptidase A inhibitory peptide C11 - striped bonito
C:Species: Sarda orientalis (striped bonito)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: JN0861
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
BioSci. Biotechnol. Biochem. 57, 1743-1744, 1993
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide
A:Reference number: JN0861; MUID:94080036; PMID:7764272
A:Accession: JN0861
A:Molecule type: protein
A:Residues: 1-6 <MAT>
A:Experimental source: liver
C:Comment: The carboxyl end is essential for the protein's expression of angiotensin I-converting enzyme
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 50.0%; Score 10; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IY 4
:
Db 2 VY 3

RESULT 5
I49421
laminin B1 - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49421
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829

Query Match 50.0%; Score 10; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IY 4
:
Db 1 VY 2

RESULT 6
I61883
protamine P1 - orangutan (fragment)
C:Species: Pongo pygmaeus (orangutan)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: I61883
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-
A:Reference number: I37013; MUID:94040810; PMID:8224908
A:Accession: I61883
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12146; NID:g38156; PIDN:CAA78130.1; PID:g4379372

Query Match 45.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 7
I37013
protamine P1 - Cercopithecus patas (fragment)
C:Species: Cercopithecus patas
C:Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I37013
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-
A:Reference number: I37013; MUID:94040810; PMID:8224908
A:Accession: I37013
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12150; NID:g22814; PIDN:CAA78134.1; PID:g4377415

Query Match 45.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 8
I84439
protamine P1 - savannah baboon (fragment)
C:Species: Papio hamadryas doquiera (savannah baboon)
C:Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I84439
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-
A:Reference number: I37013; MUID:94040810; PMID:8224908
A:Accession: I84439
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12147; NID:g38134; PIDN:CAA78131.1; PID:g4379349

Query Match 45.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||

Db 2 AR 3

RESULT 9

I40702
primase - Citrobacter diversus (fragment)
C:Species: Citrobacter diversus
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Aug-1996
C:Accession: I40702
R:Versalovic, J.; Lupski, J.R.
Mol. Microbiol. 8, 343-355, 1993
A:Title: Conservation and evolution of the rpsU-dnaG-rpoD macromolecular synthesis (MMS)
A:Reference number: I40702; MUID:93302510; PMID:8316085
A:Accession: I40702
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:L01754; NID:gl44439
C:Genetics:
A:Gene: dnaG

Query Match 45.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RI 3

||

Db 4 RI 5

RESULT 10

I39964
ribosomal protein S4 - Bacillus circulans (fragment)
C:Species: Bacillus circulans
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39964
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
A:Accession: I39964
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99041; NID:gl43471
C:Genetics:
A:Gene: rpsD

Query Match 45.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2

||

Db 2 AR 3

RESULT 11

I39966
ribosomal protein S4 - Bacillus licheniformis (fragment)
C:Species: Bacillus licheniformis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39966
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
A:Accession: I39966
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99043; NID:gl43475
C:Genetics:

A:Gene: rpsD

Query Match 45.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AR 2
||
Db 2 AR 3

RESULT 12

I39965
ribosomal protein S4 - Bacillus megaterium (fragment)
C:Species: Bacillus megaterium
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39965
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
A:Accession: I39965
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99042; NID:gl43473
C:Genetics:
A:Gene: rpsD

Query Match 45.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2

||

Db 2 AR 3

RESULT 13

PQ0009
angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N:Alternate names: ficus latex peptide 2
C:Species: Ficus carica (common fig)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C:Accession: PQ0009
R:Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A:Reference number: PQ0008
A:Accession: PQ0009
A:Molecule type: protein
A:Residues: 1-5 <MAR>
A:Experimental source: latex
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 45.0%; Score 9; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IY 4

:|

Db 1 LY 2

RESULT 14

I37027
protamine P1 - gorilla (fragment)
C:Species: Gorilla gorilla (gorilla)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C:Accession: I37027
R:Queralto, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-

A:Reference number: I37013; MUID:94040810; PMID:8224908
A:Accession: I37027
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 45.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 15
PT0568
T-cell receptor beta chain V-D-J region (141-1C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0568
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0568
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 45.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 5 AR 6

Search completed: December 12, 2002, 15:20:08
Job time : 8.8 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:38 ; Search time 4.8 Seconds
(without alignments)
34.364 Million cell updates/sec

Title: US-09-600-432-26
Perfect score: 20
Sequence: 1 ARYI 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	55.0	5	1 PSK_DAUCA	P58261 daucus caro
2	9	45.0	4	1 FYRI_ANCEL	P58706 anthopleura
3	8	40.0	6	1 UN06_CLOPA	P81351 clostridium
4	7	35.0	4	1 FAR3_HIRME	P42562 hirudo medi
5	7	35.0	4	1 FAR4_HIRME	P42563 hirudo medi
6	7	35.0	5	1 AL14_CARMA	P81817 carcinus ma
7	7	35.0	5	1 FARP_ARTTR	P41853 artiposthi
8	7	35.0	5	1 PRC2_PERAM	P01373 periplaneta
9	7	35.0	5	1 UC22_MAIZE	P80628 zea mays (m
10	7	35.0	6	1 ASP2_LACSN	P82655 lactobacilli
11	7	35.0	6	1 OVN_DEPDE	P42985 leptinotars
12	6	30.0	4	1 DCMS_PSECH	P19918 pseudomonas
13	6	30.0	6	1 CIP2_MYTED	P13737 mytilus edu
14	6	30.0	6	1 EI01_LITRU	P82096 litorea rub
15	5	25.0	4	1 FLRF_HIRME	P42561 hirudo medi
16	5	25.0	4	1 FLRN_ANCEL	P58707 anthopleura
17	5	25.0	4	1 FMRF_MAGNI	P01162 macrocallis
18	5	25.0	4	1 TUFT_HUMAN	P01858 homo sapien
19	5	25.0	5	1 EI03_LITRU	P82099 litorea rub
20	5	25.0	5	1 EI04_LITRU	P82100 litorea rub
21	5	25.0	5	1 UF01_MOUSE	P38639 mus musculu
22	5	25.0	6	1 ACPH_RABIT	P25154 onyctolagus
23	5	25.0	6	1 FARP_MONEK	P41966 moniezia ex
24	4	20.0	3	1 LUXE_VIBFI	P24272 vibrio fisc
25	4	20.0	4	1 ACHL_ACHFU	P35904 achatina fu
26	4	20.0	4	1 FKKA_ANCEL	P58705 anthopleura
27	4	20.0	5	1 BI0B_ANCEL	P12997 citrobacter
28	4	20.0	5	1 BP77_BOTIN	P30425 bothriops in
29	4	20.0	5	1 RE11_LITRU	P82070 litorea rub
30	4	20.0	5	1 RE21_LITRU	P82071 litorea rub
31	4	20.0	5	1 RE31_LITRU	P82072 litorea rub
32	4	20.0	5	1 SUGA_ACHDO	P19991 acheta dome
33	4	20.0	6	1 CIPI_MYTED	P13736 mytilus edu

34	4	20.0	6	1 LOK1_LOCFMI	P41491 locusta mig
35	4	20.0	6	1 TMOF_SARBU	P41495 sarcophaga
36	4	20.0	6	1 TRPI_PSEPU	P36414 pseudomonas
37	3	15.0	4	1 E0SI_HUMAN	P02731 homo sapien
38	3	15.0	4	1 OCPI_OCTMI	P38648 octopus min
39	3	15.0	4	1 RM01_YEAST	P36515 saccharomyc
40	3	15.0	5	1 PAP2_PARMA	P81864 pardachirus
41	3	15.0	5	1 RE32_LITRU	P82073 litorea rub
42	3	15.0	5	1 TPIS_CANFA	P54714 canis famil
43	2	10.0	3	1 GRWM_HUMAN	P01157 homo sapien
44	2	10.0	3	1 THYL_PIG	P01151 sus scrofa
45	2	10.0	4	1 DCML_PSECH	P19916 pseudomonas

ALIGNMENTS

RESULT 1
PSK_DAUCA STANDARD; PRT; 5 AA.
AC P58261:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_Taxid=4039;
RN [1]
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC STRAIN=cv. US-Harumakigosun;
RX MEDLINE=20212743; PubMed=10750705;
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
RA Kanada H., Sakagami Y.;
RT "A secreted peptide growth factor, phytosulfokine, acting as a
stimulatory factor of carrot somatic embryo formation.";
RL Plant Cell Physiol. 41:27-32(2000).
CC -I- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
EMBRYOS.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
FT MOD_RES 1 1 SULFATION.
FT MOD_RES 3 3 SULFATION.
SQ SEQUENCE 5 AA; 687 MW; 76C1BB504B300000 CRC64;

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 IY 4
DB 2 IY 3

RESULT 2
FYRI_ANCEL STANDARD; PRT; 4 AA.
AC P58706:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antho-Riamide I [Contains: Antho-Riamide II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actiniidae; Anthopleura.

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OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE
RX MEDLINE=92270459; PubMed=1821096;
RA Nother H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
RT biologically active L-3-phenylalanyl-Tyr-Arg-Ile-NH2 and its
RT des-phenylalanyl fragment Tyr-Arg-Ile-NH2.";
RL Peptides 12:1165-1173(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nother H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
RL Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
CC -I- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Neuron-specific.
DR InterPro: IPR001023; Hsp70.
KW Neuropeptide; Amidation.
FT CHAIN 1 4 ANTHO-RIAMIDE I.
FT CHAIN 2 4 ANTHO-RIAMIDE II.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 45.0%; Score 9; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RI 3
DB 3 RI 4

RESULT 3
UN06_CLOPA STANDARD; PRT; 6 AA.
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 6 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -I- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
FT NON_TER 6 6
FT SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 40.0%; Score 8; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARI 3
DB 4 AEI 6

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RESULT 4
FAR3_HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMRP-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
FT SEQUENCE 4 AA; 598 MW; 69D4073B300000000 CRC64;

Query Match 35.0%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 Y 4
DB 1 Y 1

RESULT 5
FAR4_HIRME STANDARD; PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMRP-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
FT SEQUENCE 4 AA; 616 MW; 69D4068B300000000 CRC64;

Query Match 35.0%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 Y 4
DB 1 Y 1

RESULT 6
ALI4_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

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DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Brachyura; Eubrachyura; Portunoloidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5 AMIDATION (POTENTIAL).
SQ SEQUENCE 5 AA; 586 MW; 672879DSAB300000 CRC64;

Query Match 35.0%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 Y 4
Db 1 Y 1

RESULT 7
FARP_ARTTR STANDARD; PRT; 5 AA.
AC P41853;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide RYRIF-amide.
OS Artiposiphia triangulata.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Terricola; Geoplanidae; Arthurdendyus.
OX NCBI_TaxID=132421;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=94211927; PubMed=7909164;
RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT "RYRIFamide: a turbellarian FMRamide-related peptide (FARP).";
RL Regul. Pept. 50:37-43(1994).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 5 AMIDATION.
SQ SEQUENCE 5 AA; 754 MW; 69D4004B4600000 CRC64;

Query Match 35.0%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 Y 4
Db 2 Y 2

RESULT 8
PCTC_PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and

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OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattellidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P. americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P. americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L. polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C. maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangler J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986)
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
DR PIN; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B4600000 CRC64;

Query Match 35.0%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 Y 4
Db 2 Y 2

RESULT 9
UC22_MAIZE STANDARD; PRT; 5 AA.
ID UC22_MAIZE
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
DE (Fragment).
DE Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;

```

RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernellet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
 DR Maize-2DPAGE; P80628; COLEOPTILE.
 CC MaizeDB; 123954; - 1
 FT NON_TER 5
 FT NON_TER 1
 FT NON_TER 5
 SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;
 Query Match 35.0%; Score 7; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 Y 4
 Db 1 IF 2

RESULT 10
 ASP2_LACSN STANDARD; PRT; 6 AA.
 AC P82655;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acid shock protein 2 (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 CC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 CC Lactobacillus.
 OX NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CBI;
 RX MEDLINE=21322712; PubMed=11429463;
 RA De Angelis M., Bani L., Pallini V., Cocconcelli P.S., Gobetti M.;
 RT "The acid-stress response in Lactobacillus sanfranciscensis CBI.";
 RL Microbiology 147:1863-1873(2001).
 CC -|- INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.
 FT NON_TER 6
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;
 Query Match 35.0%; Score 7; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 Y 4
 Db 4 Y 4

RESULT 11
 OVM_LEPDE STANDARD; PRT; 6 AA.
 ID OVM_LEPDE
 AC P42985;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Oviductal motility stimulating peptide (Led-OVM).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Cucujiformia; Phytophaga; Chrysomelidae; Chrysomelinae;
 CC Chrysomelinae; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA MEDLINE=91271080; PubMed=2052497;
 RX Spittael K., Schoofs L., Grauwels L., Smet H., van Damme J.,

RA Proost P., Torrekens S., de Loof A.;
 RT "Isolation, identification and synthesis of novel oviductal motility
 RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
 RT decemlineata.";
 RL Peptides 12:31-36(1991).
 CC -|- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 KW Neuropeptide; Amidation.
 FT MOD_RES 6
 FT MOD_RES 6
 SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;
 Query Match 35.0%; Score 7; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 Y 4
 Db 3 Y 3

RESULT 12
 DCMS_PSECH STANDARD; PRT; 4 AA.
 ID DCMS_PSECH
 AC P19918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit S) (CO-DH S) (Fragment).
 GN CUN5
 OS Pseudomonas carboxydohydrogena.
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Bradyrhizobium group.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydrotrophic bacteria";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -|- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -|- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -|- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
 CC -|- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR; P10146; P10146.
 KW Oxidoreductase; Iron-sulfur.
 FT NON_TER 4
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;
 Query Match 30.0%; Score 6; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AR 2
 Db 2 AK 3

RESULT 13
 CIP2_MYED STANDARD; PRT; 6 AA.
 ID CIP2_MYED
 AC P13737;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Contraction-inhibiting peptide II (MIP II).
 OS Mytilus edulis (Blue mussel).
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 CC Mytiloidea; Mytilidae; Mytilus.

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OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
CC MUSCLES.
CC -!- SIMILARITY: TO MIP I.
DR PIR: B27696; B27696.
KW Hormone; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 6;
Best Local Similarity 25.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARIY 4
DB 2 APMF 5

RESULT 14
EI01 LITRU
ID EI01 LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUPCELLULAR LOCATION: SECRETED.
KW Amphibian skin; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IY 4
DB 4 IW 5

RESULT 15
FLRF_HIRME
ID FLRF_HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FLRFamide
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;

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RN [1]
RP SEQUENCE.
RC SPECIES=H.medicalinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamlike neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRfamlike-related peptides from the kidney of the snail, Helisoma
RT trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 25.0%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
DB 3 R 3

Search completed: December 12, 2002, 15:19:18
Job time : 5.8 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:09:54 ; Search time 17 Seconds
(without alignments)
48.482 Million cell updates/sec

Title: US-09-600-432-26
Perfect score: 20
Sequence: 1 AR1Y 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	30.0	6	10 P82181	P82181 spinacia ol
2	6	30.0	6	10 P82182	P82182 spinacia ol
3	5	25.0	5	13 P83308	P83308 gallus gall
4	5	25.0	6	10 P82541	P82541 spinacia ol
5	4	20.0	5	10 Q99007	Q99007 hordeum vul
6	3	15.0	4	11 Q08433	Q08433 rattus norv
7	2	10.0	5	2 P83073	P83073 bacillus ce

ALIGNMENTS

RESULT 1
ID P82181
AC P82181; PRELIMINARY; PRT; 6 AA.

DT 01-JUN-2000 (Tremblrel. 14, Created)
DT 01-JUN-2000 (Tremblrel. 14, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001790; Ribosomal_L10.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 30.0%; Score 6; DB 10; Length 6;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2
DB 3 SR 4

RESULT 2
P82182
ID P82182 PRELIMINARY; PRT; 6 AA.
AC P82182;
DT 01-JUN-2000 (Tremblrel. 14, Created)
DT 01-JUN-2000 (Tremblrel. 14, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001790; Ribosomal_L10.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 30.0%; Score 6; DB 10; Length 6;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2
 :
 3 SR 4
 Db

RESULT 3
 P83308 ID P83308 PRELIMINARY; PRT; 5 AA.
 AC P83308;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE FMRamide-like neuropeptide (LPLRF-amide).
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=BRAIN;
 RX PubMed=613771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 antibodies to FMRamide";
 RL Nature 305:328-330(1983).
 CC -1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide.
 KW NEUROPEPTIDE.
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 25.0%; Score 5; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
 :
 4 R 4
 Db

RESULT 4
 P82541 ID P82541 PRELIMINARY; PRT; 6 AA.
 AC P82541;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 37:28455-28463(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
 CC -1- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
 CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PL. S19 BETA

CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
 CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR002222; Ribosomal_S19.
 DR Pfam: PF00203; Ribosomal_S19; PARTIAL.
 DR PRINTS: PR00975; RIBOSOMALS19; PARTIAL.
 DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 25.0%; Score 5; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
 :
 2 R 2
 Db

RESULT 5
 Q99007 ID Q99007 PRELIMINARY; PRT; 5 AA.
 AC Q99007;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE Alpha-amylase (EC 3.2.1.1) (Fragment).
 GN AMY1.
 OS Hordeum vulgare (Barley).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 CC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellic
 acid and abscisic acid in protoplasts prepared from mature barley
 aleurone layers.";
 RL Plant Mol. Biol. 16:713-721(1991).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
 CC BARLEY.
 CC EMBL; X54643; CAA38455.1; -;
 DR Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family.
 FT NON_TER 5
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DB6F00000 CRC64;

Query Match 20.0%; Score 4; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A 1
 :
 2 A 2
 Db

RESULT 6
 Q08433 ID Q08433 PRELIMINARY; PRT; 4 AA.
 AC Q08433;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JAN-1999 (TReMBLrel. 09, Last annotation update)
 DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)
 (Fragment).
 CC Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GUNN;
 RX MEDLINE=91282758; PubMed=1840486;
 RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 hyperbilirubinemic Gunn rat.";
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 ENDOGENOUS COMPOUNDS.
 CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 CC -!- BETA-D-GLUCURONOSIDE.
 CC -!- SUBCELLULAR LOCATION: MICROSOME.
 DR EMBL; S38636; AAB19259.1; -.
 KW Transferase; Glycosyltransferase; Microsome; Multigene family.
 FT NON_TER 1 1
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 15.0%; Score 3; DB 11; Length 4;
 Best Local Similarity 0.0%; Pred. No. 6.7e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 I 3
 Db 2 V 2

RESULT 7
 P83073
 ID P83073 PRELIMINARY; PRT; 5 AA.
 AC P83073;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE 88 kDa protein (Fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 6.7e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
 Db 2 K 2

Search completed: December 12, 2002, 15:18:46
 Job time : 17 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:09:28 ; Search time 27 Seconds

(without alignments)
24.676 Million cell updates/sec

Title: US-09-600-432-39

Perfect score: 25

Sequence: 1 PRARI 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 42205

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
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- 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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- 18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	5	AAW19842	Chimeric adenovirus
2	25	100.0	5	AAV28346	Beta-1 integrin ce
3	25	100.0	5	AA19066	Amino acid sequenc
4	25	100.0	6	AAV28511	Beta-1 integrin ce
5	25	100.0	6	AA19065	Amino acid sequenc
6	18	72.0	5	AA121060	Human p53 cellular
7	18	72.0	5	AAW74620	Analogue of chymot
8	18	72.0	5	AAW28512	Beta-1 integrin ce
9	18	72.0	5	AA19067	Amino acid sequenc
10	18	72.0	5	AAE24433	Transporter peptid

11	17	68.0	5	AAW50198	Sequence of oligop
12	17	68.0	5	AAW74622	Analogue of chymot
13	17	68.0	5	AAW48782	Human saliva PRP-1
14	17	68.0	5	AAW55601	T cell surface rec
15	17	68.0	5	AAW57448	DNAM-1 C-terminal
16	17	68.0	5	AAW57858	DNAM-1 C-terminal
17	17	68.0	5	AAW57858	Peptide derivative
18	17	68.0	6	AAW15886	Heparin sulfate bi
19	17	68.0	6	AAW80768	Neutrophil-activat
20	17	68.0	6	AAW50279	Fibronectin peptid
21	17	68.0	6	AAW01381	Proteoglycan bindi
22	17	68.0	6	AAW48781	Human saliva PRP-1
23	17	68.0	6	AAW55602	T cell surface rec
24	17	68.0	6	AAW57449	DNAM-1 C-terminal
25	17	68.0	6	AAW57859	DNAM-1 C-terminal
26	17	68.0	6	AAW57859	Extra cellular mat
27	17	68.0	6	AAU85707	Recombinant RSV ge
28	16	64.0	4	AAU11029	Cyclic tetrapeptid
29	16	64.0	4	AAW21664	Human IgE peptide
30	16	64.0	4	AAW42612	Human IgE mutant #
31	16	64.0	4	AAW85252	Cathepsin derived
32	16	64.0	4	AAW85383	Thrombin inhibitor
33	16	64.0	5	AAU79083	Sequence of fragme
34	16	64.0	5	AAW40816	Human growth hormo
35	16	64.0	5	AAW60156	Vasopressin fragme
36	16	64.0	5	AAW07435	C-terminal of Grow
37	16	64.0	5	AAW68079	Myelopietic proge
38	16	64.0	5	AAW23166	Terminal peptide e
39	16	64.0	5	AAW21043	Lipolytic enzyme o
40	16	64.0	5	AAW12490	Interleukin-6 anta
41	16	64.0	5	AAW20969	Human microtubule
42	16	64.0	6	AAW15732	Anticoagulant (15)
43	16	64.0	6	AAW29779	Selective factor I
44	16	64.0	6	AAW29787	Selective factor I
45	16	64.0	6	AAW29790	Selective factor I

ALIGNMENTS

RESULT 1
AAW19842
ID AAW19842 standard; Peptide; 5 AA.
XX AAW19842;
XX 26-JAN-1998 (first entry)
DT Chimeric adenovirus coat protein heparin binding motif.
DE Adenovirus; vector; coat protein; gene therapy; gene transfer;
KW human; cancer; autoimmune disease; heart disease; infection;
KW heparin.
OS Synthetic.
PN WO9720051-A2.
XX
PD 05-JUN-1997.
XX
PF 27-NOV-1996; 96WO-US19150.
XX
PR 21-AUG-1996; 96US-0701124.
PR 28-NOV-1995; 95US-0563368.
PR 21-AUG-1996; 96US-0700846.
PA (GENV-) GENVEC INC.
PI Brough DE, Kovesdi I, Wickham TJ;
DR WPI; 1997-310606/28.
XX
PT Adenoviral vectors containing chimeric coat protein - bind and enter

PT cells more efficiently, useful for gene therapy of e.g. cancer,
 XX autoimmune diseases, etc.
 PS Claim 7; Page 19; 121pp; English.
 XX This peptide is used as a universal transfer vector (UTV) sequence
 CC or as a spacer sequence in novel chimeric adenovirus coat proteins
 CC (CP), especially chimeric fibre proteins. It comprises a heparin
 CC binding motif derived from fibronectin. Claimed UTVs/spacers are
 CC given in AAW19810-11, AAW19813-25, AAW19827, AAW19829, AAW19831-32 and
 CC AAW19834-43). Claimed chimeric CPs differ from the wild-type CP by the
 CC introduction of the UTV and/or spacer at or near the C-terminus or
 CC in an exposed loop. This impacts on the chimeric CP the ability to
 CC bind to and enter cells by means of a novel cell surface binding
 CC site. Recombinant vectors comprising the chimeric CP are able to
 CC enter cells more efficiently than vectors comprising wild-type CP,
 CC especially at lower m.o.i. They are especially useful for gene
 CC therapy of e.g. cancers, genetic disorders, pathogenic infections,
 CC heart disease or autoimmune diseases.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 25; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRARI 5
 DB 1 PRARI 5
 RESULT 2
 AAY28546
 ID AAY28546 standard; peptide; 5 AA.
 AC AAY28546;
 XX
 XX 19-OCT-1999 (first entry)
 DT
 DE Beta-1 integrin cell adhesion modulator analogue #39.
 XX
 XX Beta 1 integrin dependent cell adhesion; Lipar motif; tumour;
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX
 OS Synthetic.
 XX
 PN W09937669-A1.
 XX
 XX 29-JUL-1999.
 PD
 XX 21-JAN-1999; 99WO-US01236.
 PF
 XX 12-AUG-1998; 98US-0096212.
 PR 22-JAN-1998; 98US-0072119.
 PR 12-AUG-1998; 98US-0096211.
 XX
 XX (MINU) UNIV MINNESOTA.
 PA
 PI Brienzo A, Furcht LT, McCarthy JB;
 XX
 XX WPT; 1999-469112/39.
 DR
 XX New peptides modulating betal integrin subunit dependent cell
 PT adhesion, useful to study cell adhesion e.g. alpha4betal integrin
 PT dependent adhesion important in tumour cell biology
 XX
 PS Example 11; Fig 15; 47pp; English.
 XX
 XX This peptide is used with AAY28510-Y28549 to show that peptides
 CC which modulate beta-1 integrin subunit dependent cell adhesion need a
 CC C-terminal amino acid residue (Ar) which has a side chain including an
 CC aromatic group. They also need a penultimate C-terminal amino acid
 CC residue (Lip) with an alkyl side chain group, i.e. a 'Lipar' motif.

CC Studies with these peptides have also shown that inhibiting peptides do
 CC not contain D-amino acids and that it is the presence of the ArLip motif
 CC that conveys effective betal integrin dependent cell adhesion
 CC inhibition. The beta-1 integrin subunit dependent cell adhesion is
 CC important for cell adhesion to extracellular matrix proteins, and the
 CC subunit is expressed on tumours such as melanomas. Therefore these Lipar
 CC motif containing peptides may be important in the treatment of cancer.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 25; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRARI 5
 DB 1 PRARI 5
 RESULT 3
 AAB19066
 ID AAB19066 standard; peptide; 5 AA.
 XX
 AC AAB19066;
 XX
 XX 08-FEB-2001 (first entry)
 DT
 XX Amino acid sequence of a betal-integrin inhibitor.
 DE
 XX Betal-integrin inhibitor; leukocyte mediated tissue destruction;
 KW central nervous system ischemic injury; myocardial infarction;
 KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX
 OS Synthetic.
 XX
 XX WO200056350-A2.
 PN
 XX 28-SEP-2000.
 PD
 XX 22-MAR-2000; 2000WO-US07680.
 PF
 XX 22-MAR-1999; 99US-0125634.
 PR 24-NOV-1999; 99US-0167538.
 XX
 XX (MINU) UNIV MINNESOTA.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (SENT-) SENTRON MEDICAL INC.
 XX
 XX McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
 PI Furcht LT;
 XX
 XX WPI; 2000-656062/63.
 DR
 XX Inhibition of inflammatory leukocyte mediated destruction of tissue in
 PT a patient, comprises administering a peptide inhibitor of
 PT betal-integrin, useful for treatment of e.g. cancer and osteoporosis -
 XX
 XX Claim 3; Page 38; 61pp; English.
 PS
 XX AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
 CC betal-integrin which is responsible for leukocyte mediated tissue
 CC destruction. The peptides are useful for inhibiting inflammatory
 CC leukocyte mediated destruction of tissue which occurs as a result of
 CC central nervous system (CNS) ischemic injury, myocardial infarction,
 CC angioplasty, surgical incisions, injury-related trauma, and/or
 CC transplant reperfusion, exposure to heat, cold, light, electricity
 CC and/or chemicals. They are also useful for the treatment of stroke, a
 CC burn type injury, cancer, and osteoporosis.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 25; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Gaps 0;

Matches 5; Conservative 0; Indels 0; Gaps 0;

QY 1 PRARI 5
| | | | |
Db 1 PRARI 5

RESULT 4
AAY28511
ID AAY28511 standard; peptide; 6 AA.
AC AAY28511;
XX
XX 19-OCT-1999 (first entry)
XX
XX
XX Beta-1 integrin cell adhesion modulator analogue #24.
XX
XX
XX Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
KW
XX
OS Synthetic.
XX
XX WO9937669-A1.
XX
XX 29-JUL-1999.
XX
XX 21-JAN-1999; 99WO-US01236.
XX
XX 12-AUG-1998; 98US-0096212.
PR 22-JAN-1998; 98US-0072119.
PR 12-AUG-1998; 98US-0096211.
XX
XX (MINU) UNIV MINNESOTA.
XX
XX Brienzo A. Furcht Lt, McCarthy JB;
PI
XX
XX WPI; 1999-469112/39.
XX
XX
XX New peptides modulating betal integrin subunit dependent cell
PT adhesion, useful to study cell adhesion e.g. alpha4betal integrin
PT dependent adhesion important in tumour cell biology
XX
XX Claim 6; Fig 7; 47pp; English.
XX
XX This sequence is a C-terminal tyrosine tagged peptide. This peptide
CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
CC AAY28510-Y28549 have been used to show that peptides which modulate this
CC form of cell adhesion need a C-terminal amino acid residue (Ar) which
CC has a side chain including an aromatic group, and a penultimate
CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
CC a 'lipar' motif. Studies with these peptides have also shown that
CC inhibiting peptides do not contain D-amino acids and that it is the
CC presence of the ArLip motif that conveys effective betal integrin
CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
CC cell adhesion is important for cell adhesion to extracellular matrix
CC proteins, and the subunit is expressed on tumours such as melanomas.
CC Therefore these LipAr motif containing peptides may be important in the
CC treatment of cancer.
XX
XX Sequence 6 AA;

Query Match 100.0%; Score 25; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRARI 5
| | | | |
Db 1 PRARI 5

RESULT 5
AAB19065

ID AAB19065 standard; peptide; 6 AA.
XX
AC AAB19065;
XX
XX 08-FEB-2001 (first entry)
XX
XX Amino acid sequence of a betal-integrin inhibitor.
DE
XX
XX Betal-integrin inhibitor; leukocyte mediated tissue destruction;
KW central nervous system ischemic injury; myocardial infarction;
KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
XX
OS Synthetic.
XX
XX WO200056350-A2.
XX
XX 28-SEP-2000.
XX
XX 22-MAR-2000; 2000WO-US07680.
PF
XX 22-MAR-1999; 99US-0125634.
PR 24-NOV-1999; 99US-0167538.
PR
XX (MINU) UNIV MINNESOTA.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (SENT-) SENTRON MEDICAL INC.
XX
XX McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
PI Furcht Lt;
PI
XX WPI; 2000-656062/63.
DR
XX
XX Inhibition of inflammatory leukocyte mediated destruction of tissue in
PT a patient, comprises administering a peptide inhibitor of
PT betal-integrin, useful for treatment of e.g. cancer and osteoporosis
XX
XX Claim 3; Page 38; 6lpp; English.
XX
XX AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
CC betal-integrin which is responsible for leukocyte mediated tissue
CC destruction. The peptides are useful for inhibiting inflammatory
CC leukocyte mediated destruction of tissue which occurs as a result of
CC central nervous system (CNS) ischemic injury, myocardial infarction,
CC angioplasty, surgical incisions, injury-related trauma, and/or
CC transplant reperfusion, exposure to heat, cold, light, electricity
CC and/or chemicals. They are also useful for the treatment of stroke, a
CC burn type injury, cancer, and osteoporosis.
XX
XX Sequence 6 AA;

Query Match 100.0%; Score 25; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRARI 5
| | | | |
Db 1 PRARI 5

RESULT 6
AAY21060
ID AAY21060 standard; Protein; 5 AA.
XX
XX AAY21060;
XX
XX 22-JUL-1999 (first entry)
XX
XX Human p53 cellular tumour antigen mutant protein fragment 7.
XX
XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;

KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN WO9845322-A2.
 PN 15-OCT-1998.
 PD 02-APR-1998; 98WO-IB00705.
 PF 10-APR-1997; 97US-0043163.
 PR (UYUT-) RIJKSUNIV UTRECHT.
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX Burbach JPH, Grosveld FG, Van Leeuwen FW;
 XX WPI; 1998-609901/51.
 DR N-PSDB; AAX75765.
 XX
 XX Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 PT RNA
 XX
 XX Disclosure; Figure 14; 258pp; English.
 XX
 XX This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX
 SQ Sequence 5 AA;
 Query Match 72.0%; Score 18; DB 19; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRAR 4
 DB 2 PRSR 5
 XX
 XX RESULT 7
 XX ANW74620
 ID ANW74620 standard; peptide; 5 AA.
 AC ANW74620;
 XX
 XX 21-DEC-1998 (first entry)
 DT

XX Analogue of chymotrypsin-cleaved suPAR peptide 7.
 DE Human; urokinase receptor; uPAR; soluble uPAR; suPAR; chymotrypsin;
 KW cleavage; cancer; autoimmune disease; inflammatory disorder;
 KW wound healing; antigen; vaccination; HIV.
 XX
 OS Homo sapiens.
 PN WO9842733-A1.
 PN 01-OCT-1998.
 PD 18-MAR-1998; 98WO-EP01547.
 PF 20-MAR-1997; 97US-0041112.
 PR (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
 PA (UYMI-) UNIV MILAN STUDI.
 XX Blasi F, Fazloli F, Nicolai S, Resnati M;
 XX WPI; 1998-531946/45.
 XX New soluble urokinase receptor products obtained by chymotrypsin
 PT cleavage - useful for, e.g. treating cancers, autoimmune diseases
 PT and inflammatory disorders or for stimulating wound healing
 PT
 XX Disclosure; Page 13; 59pp; English.
 PS
 XX This is the nucleotide sequence of a functional analogue of the
 CC chymotrypsin-cleaved human soluble urokinase receptor (suPAR)
 CC peptide used in the method of the invention. In this process suPAR
 CC products obtained by chymotrypsin cleavage is used to treat cancer,
 CC autoimmune disease, inflammatory disorders, suPAR peptide or its
 CC functional peptide may be used for stimulating or increasing wound
 CC healing, stimulating the kinase activity. A peptide comprising the
 CC sequence SRSRI or its functional analogue may be used for stimulating
 CC or increasing, e.g. the chemotactic activity of a cell, a local
 CC inflammatory response and anti-tumour immunity in autologous bone
 CC marrow transplantation treatment of an individual, e.g. a human
 CC patient, who is immunodeficient. These products may also be used for
 CC increasing the immunogenicity of antigens in vaccination, e.g. against
 CC viral infections such as HIV infection.
 XX
 SQ Sequence 5 AA;
 Query Match 72.0%; Score 18; DB 19; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRAR 4
 DB 1 PRSR 4
 XX
 XX RESULT 8
 XX AAY28512
 ID AAY28512 standard; peptide; 5 AA.
 XX
 AC AAY28512;
 XX
 XX 19-OCT-1999 (first entry)
 DT
 XX Beta-1 integrin cell adhesion modulator analogue #25.
 DE
 XX Beta 1 integrin dependent cell adhesion; LipAR motif; tumour;
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX
 OS Synthetic.
 XX WO9937669-A1.
 PN
 XX

PD 29-JUL-1999.
 XX
 PF 21-JAN-1999; 99WO-US01236.
 XX
 PR 12-AUG-1998; 98US-0096212.
 PR 22-JAN-1998; 98US-0072119.
 PR 12-AUG-1998; 98US-0096211.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Brienzo A, Furcht LT, McCarthy JB;
 XX
 DR WPI; 1999-469112/39.
 XX
 PT New peptides modulating betal integrin subunit dependent cell
 PT adhesion, useful to study cell adhesion e.g. alpha4betal integrin
 PT dependent adhesion important in tumour cell biology
 XX
 PS Claim 6; Fig 7; 47pp; English.
 XX
 CC This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAY28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which
 CC has a side chain including an aromatic group, and a penultimate
 CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
 CC a 'LipAr' motif. Studies with these peptides have also shown that
 CC inhibiting peptides do not contain D-amino acids and that it is the
 CC presence of the ArLip motif that conveys effective betal integrin
 CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
 CC cell adhesion is important for cell adhesion to extracellular matrix
 CC proteins, and the subunit is expressed on tumours such as melanomas.
 CC Therefore these Lipar motif containing peptides may be important in the
 CC treatment of cancer.
 XX
 SQ Sequence 5 AA;
 Query Match 72.0%; Score 18; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 RARI 5
 DB 1 RARI 4
 DE
 DE Amino acid sequence of a betal-integrin inhibitor.
 XX
 KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
 KW central nervous system ischemic injury; myocardial infarction;
 KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX
 OS Synthetic.
 XX
 PN WO200056350-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US07680.
 XX
 PR 22-MAR-1999; 99US-0125634.
 PR 24-NOV-1999; 99US-0167538.
 XX
 PA (MINU) UNIV MINNESOTA.

PA (TEXA) UNIV TEXAS SYSTEM.
 PA (SENT-) SENTRON MEDICAL INC.
 XX
 PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
 PI Furcht LT;
 XX
 DR WPI; 2000-656062/63.
 XX
 PT Inhibition of inflammatory leukocyte mediated destruction of tissue in
 PT a patient, comprises administering a peptide inhibitor of
 PT betal-integrin, useful for treatment of e.g. cancer and osteoporosis -
 XX
 PS Claim 3; Page 38; 61pp; English.
 XX
 CC AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
 CC betal-integrin which is responsible for leukocyte mediated tissue
 CC destruction. The peptides are useful for inhibiting inflammatory
 CC leukocyte mediated destruction of tissue which occurs as a result of
 CC central nervous system (CNS) ischemic injury, myocardial infarction,
 CC angioplasty, surgical incisions, injury-related trauma, and/or
 CC transplant reperfusion, exposure to heat, cold, light, electricity
 CC and/or chemicals. They are also useful for the treatment of stroke, a
 CC burn type injury, cancer, and osteoporosis.
 XX
 SQ Sequence 5 AA;
 Query Match 72.0%; Score 18; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 RARI 5
 DB 1 RARI 4
 DE
 DE Transporter peptide, T7.
 XX
 KW Transporter peptide; therapy; colon cancer; neurodegenerative disorder;
 KW diabetes; respiratory ailment; cardiplegia; viral infection; cytostatic;
 KW virucide; neuroprotective.
 XX
 OS Unidentified.
 XX
 PN WO200231109-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 15-OCT-2001; 2001WO-IB02423.
 XX
 PR 13-OCT-2000; 2000US-240313P.
 XX
 PA (UYIA-) UNIV LAUSANNE.
 XX
 PI Bonny C;
 XX
 DR WPI; 2002-479626/51.
 XX
 PT Novel transporter peptide useful for the intracellular delivery of
 PT biological effectors for treating diabetes, colon cancer, respiratory
 PT ailments, neurodegenerative disorders, cardiplegia, and viral
 PT infections -
 XX
 PS Claim 35; Page 26; 50pp; English.
 XX
 CC The present invention relates to novel transporter peptides with the

CC capacity to facilitate transport of an effector across a biological
 CC membrane. Sequences of the invention are useful for translocating an
 CC effector into the cytoplasm and nucleus of a eukaryotic cell preferably
 CC a human cell. They are also useful for increasing the intracellular
 CC concentration of an effector within a eukaryotic cell, preferably human
 CC cell. Transporter peptides of the invention are useful for transporting
 CC an effector across a biological membrane, for targeting various cell
 CC types for the intracellular delivery of drugs and therapeutic agents
 CC and for increasing the biological activity of the effector to which
 CC it is coupled. Pharmaceutical compositions comprising the transporter
 CC peptides are useful for treating or preventing diseases such as colon
 CC cancer, diabetes, respiratory ailments, neurodegenerative disorders,
 CC cardioplegia and viral infections. The present sequence is a transporter
 CC peptide of the invention. This peptide can be translocated across a
 CC membrane of lung cells.

XX Sequence 5 AA;

Query Match 72.0%; Score 18; DB 23; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRAR 4
 |||
 Db 1 PRSR 4

RESULT 11

AAFP50198
 ID AAFP50198 standard; peptide; 5 AA.

XX AC AAFP50198;

XX 17-OCT-1991 (first entry)

XX DE Sequence of oligopeptide 1 specific to the beta-subunit of human
 DE chorionic gonadotropin (HCG).

XX KW Contraception; assay; pregnancy test; luteinising hormone;
 KW human chorionic gonadotropin.

XX OS Homo sapiens.

XX PN EP142387-A.

XX PD 22-MAY-1985.

XX PF 23-AUG-1984; 84EP-0401710.

XX PR 26-AUG-1983; 83EP-0401714.

XX PR 23-AUG-1984; 84EP-0401710.

XX PA (ANDA-) ANDA BIOLOGICALS.

XX PI Maes RP;

XX WPI; 1985-124152/21.

XX PT Prepn. of anti-HCG and anti-LH vaccines - by use of
 PT oligo-peptide(s) specific to beta-sub-unit of LH and HCG

XX PS Claim 1; Page 17; 22pp; English.

XX CC Oligopeptides AAP50198-P50205, specific to the beta-subunit of LH and
 CC of HCG, located near cysteine groups, are used in a claimed process
 CC for the preparation of anti-HCG and anti-LH vaccines. The vaccines
 CC are characterised in that these oligopeptides are complexed upon
 CC themselves and between themselves by disulphur bridges, upon their
 CC own beta-subunit of HCG and LH or upon oligopeptides containing
 CC cysteine whose AA chain is common to LH and HCG, namely the peptides
 CC in AAP50208-P50212. Through sulphur bridges the specific oligopeptides
 CC are administered by injection in vaccines to cause prodn. of
 CC antibodies so that a contraceptive effect is achieved; and the

CC antibodies are also useful in assays for HCG and LH in body fluids.

XX SQ Sequence 5 AA;

Query Match 68.0%; Score 17; DB 6; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRAR 4
 |||
 Db 1 PRCR 4

RESULT 12

AAW74622
 ID AAW74622 standard; peptide; 5 AA.

XX AC AAW74622;

XX 21-DEC-1998 (first entry)

XX DE Analogue of chymotrypsin-cleaved supAR peptide 9.

XX KW Human; urokinase receptor; uPAR; soluble uPAR; supAR; chymotrypsin;
 KW cleavage; cancer; autoimmune disease; inflammatory disorder;
 KW wound healing; antigen; vaccination; HIV.

XX OS Homo sapiens.

XX PN WO9842733-A1.

XX PD 01-OCT-1998.

XX PF 18-MAR-1998; 98WO-EP01547.

XX PR 20-MAR-1997; 97US-0041112.

XX PA (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.

XX PA (UYMI-) UNIV MILAN STUDI.

XX PI Blasi F, Fazioli F, Nicolai S, Resnati M;

XX WPI; 1998-531946/45.

XX PT New soluble urokinase receptor products obtained by chymotrypsin
 PT cleavage - useful for, e.g. treating cancers, autoimmune diseases
 PT and inflammatory disorders or for stimulating wound healing

XX PS Disclosure; Page 13; 59pp; English.

XX CC This is the nucleotide sequence of a functional analogue of the
 CC chymotrypsin-cleaved human soluble urokinase receptor (supAR)
 CC peptide used in the method of the invention. In this process supAR
 CC products obtained by chymotrypsin cleavage is used to treat cancer,
 CC autoimmune disease, inflammatory disorders, supAR peptide or its
 CC functional peptide may be used for stimulating or increasing wound
 CC healing, stimulating the kinase activity. A peptide comprising the
 CC sequence SRSR or its functional analogue may be used for stimulating
 CC or increasing, e.g. the chemotactic activity of a cell, a local
 CC inflammatory response and anti-tumour immunity in autologous bone
 CC marrow transplantation treatment of an individual, e.g. a human
 CC patient, who is immunodeficient. These products may also be used for
 CC increasing the immunogenicity of antigens in vaccination, e.g. against
 CC viral infections such as HIV infection.

XX SQ Sequence 5 AA;

Query Match 68.0%; Score 17; DB 19; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRAR 4
 |||

```

Db      1 PRGR 4
RESULT 13
AAB48782
ID AAB48782 standard; peptide; 5 AA.
XX
AC AAB48782;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human saliva PRP-1 fragment (residues 104-108), SEQ ID NO:12.
XX
KW Human; PRP-1; proline-rich protein; saliva; dental caries;
KW Chromosome 12p13.2; arginine catabolism; ammonia production;
KW pH increase; oral bacterium; caries prevention.
XX
OS Homo sapiens.
XX
PN WO2000069890-A1.
XX
PD 23-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-SF00930.
XX
PR 17-MAY-1999; 99SE-0001773.
XX
PA (STRO/) STROEMBERG N.
PA (JOHA/) JOHANSSON I.
XX
PI Stroemberg N, Johansson I;
XX
XX WPI; 2001-031923/04.
XX
PT New oligopeptides comprising 2 arginine residues from degradation of
PT proline-rich proteins, useful for preventing dental caries -
XX
PS Claim 4; Page 24; 36pp; English.
XX
CC The invention relates to human PRP-1-derived oligopeptides (AAB48771-
CC AAB48783) which contain at least two arginine residues and which protect
CC against dental caries. PRPs (proline-rich proteins) are salivary
CC proteins encoded by six clustered genes on chromosome 12p13.2 and are
CC potential determinants of a person's susceptibility to dental caries.
CC PRPs are degraded by Actinomyces and Streptococcus species to small
CC peptide fragments. These are metabolised by oral bacteria for
CC nutritional purposes, with certain bacterial species generating ammonia
CC via the catabolism of arginine. The peptides of the invention, being
CC arginine-rich, can also be converted to ammonia by these bacteria. The
CC ammonia thus formed raises the pH at the dental surface, thereby
CC protecting the teeth against caries. Sequences AAB48771-B48783 represent
CC the PRP-1-derived oligopeptides of the invention.
XX
SQ Sequence 5 AA;
XX
Query Match 68.0%; Score 17; DB 22; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PRAR 4
DB 2 PRGR 5
XX
RESULT 14
AAB55601
ID AAB55601 standard; Peptide; 5 AA.
XX
AC AAB55601;
XX
DT 07-MAR-2001 (first entry)
XX
DE T cell surface receptor PDZ domain sequence #72.
XX
XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
KW allergy; asthma; multiple sclerosis; cancer; infection.
XX
OS Synthetic.
XX
PN WO2000069896-A2.
XX
PD 23-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US13161.
XX
PR 14-MAY-1999; 99US-0134114.
PR 14-MAY-1999; 99US-0134117.
PR 14-MAY-1999; 99US-0134118.
PR 21-OCT-1999; 99US-0160860.
PR 29-OCT-1999; 99US-0162498.
PR 13-DEC-1999; 99US-0170453.
PR 14-JAN-2000; 2000US-0176195.
PR 14-FEB-2000; 2000US-0182296.
PR 11-APR-2000; 2000US-0196460.
PR 11-APR-2000; 2000US-0196527.
XX
PA (ARBO-) ARBOR VITA CORP.
XX
PI Lu PS;
XX
XX WPI; 2001-080245/09.
XX
PT Modulating a biological function of an endothelial cell or
PT hematopoietic cell, useful for treating autoimmune diseases and
PT infectious diseases, by administering an antagonist that inhibits
PT binding between a PDZ protein and a PL protein -
XX
PS Disclosure; Page 87-94; 141pp; English.
XX
CC The present invention relates to a new method for modulating a
CC biological function of an endothelial cell or hematopoietic cell. The
CC method involves introducing into a cell, an antagonist that inhibits
CC binding between a PDZ protein and a PL protein. The inhibitor is used
CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
CC disease. It may also be used to prevent transplantation rejection of
CC a solid organ transplant. The method may also be used in the treatment
CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
CC graft rejection, transplantation rejection), atherosclerosis, cancers,
CC infectious diseases, ischemia, vasculitis and Crohn's disease.
XX
SQ Sequence 5 AA;
XX
Query Match 68.0%; Score 17; DB 22; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 PRARI 5
DB 1 PKTRV 5
XX
RESULT 15
AAB57448
ID AAB57448 standard; Peptide; 5 AA.
XX
AC AAB57448;
XX
DT 12-MAR-2001 (first entry)
XX
DE DNAM-1 C-terminal core sequence #2.
XX
KW Endothelial cell; haematopoietic cell; PDZ domain protein;
KW PL domain protein; leukocyte activation; T cell surface receptor;

```

KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.

XX WO200069897-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13166.

XX 14-MAY-1999; 99US-0134114.

PR 14-MAY-1999; 99US-0134117.

PR 14-MAY-1999; 99US-0134118.

PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.

PR 13-DEC-1999; 99US-0170453.

PR 14-JAN-2000; 2000US-0176195.

PR 14-FEB-2000; 2000US-0182236.

PR 11-APR-2000; 2000US-0196460.

PR 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-025003/03.

XX New inhibitors of binding of a PDZ protein and PL protein for
 PT inhibiting T cell-mediated response by hematopoietic cells, or for
 PT treating diseases characterized by inflammatory and humoral immune
 PT responses, e.g. inflammation, cancer -
 XX
 PS Disclosure; Page 88; 139pp; English.
 CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or haematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present invention is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypal proteins: PSD95, Drosophila large disc
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.

XX Sequence 5 AA;

Query Match 68.0%; Score 17; DB 22; Length 5;
 Best Local Similarity 40.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PRARI 5

Db 1 PKTRV 5

Search completed: December 12, 2002, 15:17:16
 Job time : 27 secs

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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:15:23 ; Search time 9.5 Seconds
(without alignments)
15.486 Million cell updates/sec

Title: US-09-600-432-39

Perfect score: 25

Sequence: 1 PRARI 5

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 32749

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	25	100.0	5	4	US-09-101-751A-57
2	18	72.0	4	2	US-08-480-133A-15
3	18	72.0	4	3	US-09-008-308-30
4	18	72.0	5	4	US-09-381-244B-13
5	17	68.0	5	1	US-08-375-879-4
6	17	68.0	5	3	US-09-125-517A-42
7	17	68.0	5	4	US-09-284-625-6
8	17	68.0	5	4	US-09-381-244B-15
9	17	68.0	6	3	US-09-125-517A-8
10	17	68.0	6	4	US-09-057-052-7
11	16	64.0	4	1	US-08-240-514-5
12	16	64.0	4	2	US-08-612-302A-5
13	16	64.0	4	2	US-08-637-759B-421
14	16	64.0	4	2	US-08-232-539D-46
15	16	64.0	4	3	US-08-871-355A-421
16	16	64.0	4	3	US-08-466-151-59
17	16	64.0	4	3	US-09-008-308-29
18	16	64.0	4	4	US-08-974-549A-541
19	16	64.0	4	4	US-08-466-163B-59
20	16	64.0	4	4	US-09-201-945-421
21	16	64.0	5	1	US-08-095-162-22
22	16	64.0	5	1	US-08-021-608D-21
23	16	64.0	5	1	US-08-470-220A-22
24	16	64.0	5	1	US-08-458-997-2
25	16	64.0	5	1	US-08-726-160-21
26	16	64.0	5	1	US-07-923-724-19
27	16	64.0	5	2	US-08-609-426A-19

28 16 64.0 5 2 US-08-374-652C-11 Sequence 11, Appl
29 16 64.0 5 3 US-08-967-374-22 Sequence 22, Appl
30 16 64.0 5 3 US-08-208-264A-36 Sequence 36, Appl
31 16 64.0 5 3 US-09-008-308-9 Sequence 9, Appl
32 16 64.0 5 4 US-09-421-097-36 Sequence 36, Appl
33 16 64.0 5 4 US-09-505-991-22 Sequence 22, Appl
34 16 64.0 6 1 US-07-859-281C-18 Sequence 18, Appl
35 16 64.0 6 1 US-08-022-381A-19 Sequence 2, Appl
36 16 64.0 6 1 US-08-049-195A-2 Sequence 19, Appl
37 16 64.0 6 1 US-08-475-827A-19 Sequence 19, Appl
38 16 64.0 6 1 US-08-704-170-89 Sequence 89, Appl
39 16 64.0 6 1 US-08-458-997-3 Sequence 3, Appl
40 16 64.0 6 1 US-08-458-997-5 Sequence 5, Appl
41 16 64.0 6 1 US-08-458-997-8 Sequence 8, Appl
42 16 64.0 6 1 US-08-458-997-9 Sequence 9, Appl
43 16 64.0 6 1 US-08-458-997-10 Sequence 10, Appl
44 16 64.0 6 1 US-08-458-997-11 Sequence 11, Appl
45 16 64.0 6 1 US-08-458-997-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-101-751A-57
; Sequence 57, Application US/09101751A
; Patent No. 6465253
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS
; FILE REFERENCE: 85710
; CURRENT APPLICATION NUMBER: US/09/101,751A
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (..)
; OTHER INFORMATION: Description of Unknown Organism: Artificial
; OTHER INFORMATION: Sequence

Query Match 100.0%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRARI 5
| | | | |

Db 1 PRARI 5

RESULT 2
US-08-480-133A-15
; Sequence 15, Application US/08480133A
; Patent No. 5840691
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: McCarthy, James B.
; APPLICANT: Wahl, Sharon M.

APPLICANT: Allen, Janice B.
APPLICANT: Billups, Kevin L.
APPLICANT: Everett, Jeffrey E.
TITLE OF INVENTION: Method for Treating Inflammatory
TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5840691west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,133A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,903
FILING DATE: 21-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,296
FILING DATE: 10-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles C.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 600-308US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-08-480-133A-15
Query Match 72.0%; Score 18; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RARI 5
DB 1 RARI 4
RESULT 3
US-09-008-308-30
Sequence 30, Application US/09008308
Patent No. 6080575
GENERAL INFORMATION:
APPLICANT: Heidtmann, Hans H.
APPLICANT: Mueller, Rolf
APPLICANT: Sedlacek, Hans-Harald
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
TITLE OF INVENTION: ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES, AND
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,308
FILING DATE: 16-JAN-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 197 01 141.1
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 026083/0189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-008-308-30
Query Match 72.0%; Score 18; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RARI 5
DB 1 RARI 4
RESULT 4
US-09-381-244B-13
Sequence 13, Application US/09381244B
Patent No. 6462170
GENERAL INFORMATION:
APPLICANT: BLASI, Francesco
APPLICANT: FAZIOLI, Francesca
APPLICANT: RESNATI, Massimo
APPLICANT: NICOLAI, Sidenius
TITLE OF INVENTION: upAR Mimicking Peptide
FILE REFERENCE: 0471-0143P
CURRENT APPLICATION NUMBER: US/09/381,244B
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: PCT/EP98/01547
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 5
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
OTHER INFORMATION: peptide analogue of the human upAR
US-09-381-244B-13
Query Match 72.0%; Score 18; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 PRAR 4
DB 1 PRSR 4
RESULT 5

```
US-08-375-879-4
; Sequence 4, Application US/08375879
; Patent No. 5614608
; GENERAL INFORMATION:
; APPLICANT: Krchnak, Viktor
; APPLICANT: Lebl, Michal
; APPLICANT: Seligman, Bruce
; TITLE OF INVENTION: Apparatus and Method for Multiple
; TITLE OF INVENTION: Synthesis of Organic Compounds on Polymer Support
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/375,879
; FILING DATE: 20-JAN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18872
; REFERENCE/DOCKET NUMBER: 7156-068
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-375-879-4

Query Match 68.0%; Score 17; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRAR 4
Db 2 PRGR 5

RESULT 6
US-09-125-517A-42
; Sequence 42, Application US/09125517A
; Patent No. 6087336
; GENERAL INFORMATION:
; APPLICANT: Cotton, Ronald
; APPLICANT: Edwards, Philip Neil
; TITLE OF INVENTION: Luke, Richard William Arthur
; TITLE OF INVENTION: Peptide Derivatives
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth St., N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,517A
; FILING DATE: 20-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9603855.9
; FILING DATE: 23-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9620819.4
; FILING DATE: 05-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1991-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-125-517A-42

Query Match 68.0%; Score 17; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
Db 2 RARV 5

RESULT 7
US-09-284-625-6
; Sequence 6, Application US/09284625
; Patent No. 6207644
; GENERAL INFORMATION:
; APPLICANT: Luke, Richard William
; APPLICANT: Cotton, Richard
; TITLE OF INVENTION: Peptide Analogues Containing a 7-membered Lactam Ring
; FILE REFERENCE: 1991-169
; CURRENT APPLICATION NUMBER: US/09/284,625
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: PCT/GB97/02837
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: GB 96218367
; PRIOR FILING DATE: 1996-10-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-284-625-6

Query Match 68.0%; Score 17; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
Db 2 RARV 5

RESULT 8
US-09-381-244B-15
; Sequence 15, Application US/09381244B
; Patent No. 6462170
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; GENERAL INFORMATION:
; APPLICANT: BLASI, Francesco
; APPLICANT: FAZIOLI, Francesca
; APPLICANT: RESNATI, Massimo
; APPLICANT: NICOLAI, Sidenius
; TITLE OF INVENTION: uPAR Mimicking Peptide
; FILE REFERENCE: 0471-0143P
; CURRENT APPLICATION NUMBER: US/09/381,244B
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/EP98/01547
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: peptide analogue of the human uPAR
US-09-381-244B-15

Query Match 68.0%; Score 17; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRAR 4
DB 1 PRGR 4

RESULT 9
US-09-125-517A-8
; Sequence 8, Application US/09125517A
; Patent No. 6087336
; GENERAL INFORMATION:
; APPLICANT: Cotton, Ronald
; APPLICANT: Edwards, Philip Neil
; APPLICANT: Luke, Richard William Arthur
; TITLE OF INVENTION: Peptide Derivatives
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth St., N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,517A
; FILING DATE: 20-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9603855.9
; FILING DATE: 23-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9620819.4
; FILING DATE: 05-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1991-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: PRT
; STRANDEDNESS:
; TOPOLOGY:
; US-09-057-052-7

Query Match 68.0%; Score 17; DB 4; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
DB 2 RARV 5

RESULT 10
US-09-057-052-7
; Sequence 7, Application US/09057052
; Patent No. 6331422
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Schense, Jason
; TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for
; TISSUE ENGINEERING
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vinson & Elkins L.L.P.
; STREET: 600 Congress Avenue, Suite 2700
; CITY: Austin
; STATE: Texas
; COUNTRY: US
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,052
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,143
; FILING DATE: 03-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: CAL430.23000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 495-8400
; TELEFAX: (512) 495-8612
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-057-052-7

Query Match 68.0%; Score 17; DB 4; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
DB 2 RARV 5

LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "5-Phenylpentanoyl-Ala"
FEATURE:
NAME/KEY: Peptide
LOCATION: 6
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note=
OTHER INFORMATION: "[(S)-2-((R)-3-amino-2-oxopyrrolidin-1-yl)propanoyl]-Gly-4"
US-09-125-517A-8
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Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
 |||
 Db 3 RARV 6

RESULT 11
 US-08-240-514-5
 ; Sequence 5, Application US/08240514
 ; Patent No. 5670347
 ; GENERAL INFORMATION:
 ; APPLICANT: GOPAL, T. Venkat
 ; TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 11-MAY-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 73521/102/CLIN
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: amino acid
 ; LENGTH: 4
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-240-514-5

Query Match 64.0%; Score 16; DB 1; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRAR 4
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 Db 1 PRKR 4

RESULT 12
 US-08-612-302A-5
 ; Sequence 5, Application US/08612302A
 ; Patent No. 5811297
 ; Patent No. 5811297 5780297
 ; GENERAL INFORMATION:
 ; APPLICANT: GOPAL, T. Venkat
 ; TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: One Westlakes, Berwyn
 ; CITY: Valley Forge
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612.302A
 ; FILING DATE: 7 March 1996
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Amzel, Viviana
 ; REGISTRATION NUMBER: 30,930
 ; REFERENCE/DOCKET NUMBER: AMBA-020
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 407-0700
 ; TELEFAX: (610) 407-0701
 ; TELEX: n.a.
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: n.a.
 ; TOPOLOGY: n.a.
 ; US-08-612-302A-5

Query Match 64.0%; Score 16; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRAR 4
 |||
 Db 1 PRKR 4

RESULT 13
 US-08-637-759B-421
 ; Sequence 421, Application US/08637759B
 ; Patent No. 5876931
 ; GENERAL INFORMATION:
 ; APPLICANT: David William Holden
 ; TITLE OF INVENTION: Identification of Genes
 ; NUMBER OF SEQUENCES: 501
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 2800 One Atlantic Center
 ; STREET: 1201 West Peachtree Street
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: USA
 ; ZIP: 30309-3450
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/637,759B
 ; FILING DATE: 03-MAY-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB95/02875
 ; FILING DATE: 11-DEC-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31,284
 ; REFERENCE/DOCKET NUMBER: RPMS 101
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (404) 873-8794
 ; TELEFAX: (404) 873-8795
 ; INFORMATION FOR SEQ ID NO: 421:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid

;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
US-08-637-759B-421

Query Match 64.0%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRA 3
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Db 2 PRA 4

RESULT 14

US-08-232-539D-46
; Sequence 46, Application US/08232539D
; Patent No. 5965709

;; GENERAL INFORMATION:
;; APPLICANT: Presta, Leonard G.
;; APPLICANT: Jardieu, Paula M.
;; TITLE OF INVENTION: Ige Antagonists
;; NUMBER OF SEQUENCES: 60
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/232,539D
;; FILING DATE: 21-Apr-1994
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/178583
;; FILING DATE: 07-JAN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/744768
;; FILING DATE: 14-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svoboda, Craig G.
;; REGISTRATION NUMBER: 39,044
;; REFERENCE/DOCKET NUMBER: P0718P3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1489
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 46:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear

US-08-232-539D-46

Query Match 64.0%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRA 3
|||
Db 1 PRA 3

RESULT 15

US-08-871-355A-421
; Sequence 421, Application US/08871355A
; Patent No. 6015669

;; GENERAL INFORMATION:
;; APPLICANT: David William Holden
;; TITLE OF INVENTION: Identification of Genes
;; NUMBER OF SEQUENCES: 501
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Patrea L. Pabst
;; STREET: 2800 One Atlantic Center
;; CITY: Atlanta
;; STATE: Georgia
;; COUNTRY: USA
;; ZIP: 30309-3450
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/871,355A
;; FILING DATE: 09-JUN-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB95/02875
;; FILING DATE: 11-DEC-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: RPMS 101 CON
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404) 873-8794
;; INFORMATION FOR SEQ ID NO: 421:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
US-08-871-355A-421

Query Match 64.0%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRA 3
|||
Db 2 PRA 4

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Job time : 9.5 secs

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OM protein - protein search, using sw model.

Run on: December 12, 2002, 15:17:24 ; Search time 5.25 seconds
(without alignments)
15.869 Million cell updates/sec

Title: US-09-600-432-39

Perfect score: 25

Sequence: 1 PRARI 5

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	17	68.0	6	10	US-09-887-469-20
5	16	64.0	4	10	US-09-802-077-59
6	16	64.0	4	10	US-09-802-096-59
7	16	64.0	6	12	US-10-036-418-17
8	16	64.0	6	12	US-10-036-418-18
9	15	60.0	5	10	US-09-800-433-5
10	14	56.0	5	10	US-09-800-433-7
11	14	56.0	5	10	US-09-977-831-19
12	14	56.0	5	10	US-09-947-387-47
13	14	56.0	6	9	US-09-823-823-66
14	14	56.0	6	10	US-09-904-539A-3
15	14	56.0	6	10	US-09-823-823-66
16	14	56.0	6	12	US-10-066-151-6
17	14	56.0	4	12	US-10-041-030-25
18	13	52.0	4	12	US-10-041-030-25
19	13	52.0	5	9	US-10-104-019-43

20	13	52.0	5	10	US-09-803-126-18
21	13	52.0	5	10	US-09-953-657-4
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23	13	52.0	6	10	US-09-113-696B-21
24	13	52.0	6	10	US-09-808-832-17
25	13	52.0	6	10	US-09-808-832-89
26	13	52.0	6	10	US-09-808-387-45
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30	12	48.0	4	10	US-09-802-077-60
31	12	48.0	4	10	US-09-802-096-60
32	12	48.0	4	10	US-09-040-518-8
33	12	48.0	4	10	US-09-956-425-14
34	12	48.0	4	10	US-09-804-733A-24
35	12	48.0	4	10	US-09-873-737A-21
36	12	48.0	4	10	US-09-933-497B-37
37	12	48.0	4	10	US-09-765-614B-30
38	12	48.0	4	10	US-09-925-715-26
39	12	48.0	4	10	US-09-977-831-12
40	12	48.0	4	10	US-09-977-831-12
41	12	48.0	4	10	US-09-984-183-20
42	12	48.0	4	10	US-09-819-136-6
43	12	48.0	4	10	US-09-871-974-1
44	12	48.0	4	10	US-09-871-974-12
45	12	48.0	4	10	US-09-947-387-48

ALIGNMENTS

RESULT 1
US-09-010-714-10
; Sequence 10, Application US/09010714
; Patent No. US20020012942A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; APPLICANT: Iida, Joji
; TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
; FILE REFERENCE: 600.332US01
; CURRENT APPLICATION NUMBER: US/09/010,714
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-010-714-10

Query Match 72.0%; Score 18; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
Db 1 RARI 4

RESULT 2

US-09-977-831-30
; Sequence 30, Application US/09977831
; Patent No. US20020120100A1
; GENERAL INFORMATION:
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 Transporter peptides
; CURRENT APPLICATION NUMBER: US/09/977,831
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/240,315

Sequence 18, Appl
GENERAL INFORMA
Sequence 28, Appl
Sequence 21, Appl
Sequence 17, Appl
Sequence 89, Appl
Sequence 45, Appl
Sequence 8, Appl
Sequence 13, Appl
Sequence 108, Appl
Sequence 60, Appl
Sequence 8, Appl
Sequence 14, Appl
Sequence 24, Appl
Sequence 21, Appl
Sequence 37, Appl
Sequence 30, Appl
Sequence 26, Appl
Sequence 12, Appl
Sequence 16, Appl
Sequence 20, Appl
Sequence 6, Appl
Sequence 1, Appl
Sequence 12, Appl
Sequence 48, Appl

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; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-09-977-831-30

Query Match      72.0%; Score 18; DB 10; Length 5;
Best Local Similarity 75.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRAR 4
Db 1 PRSR 4

RESULT 3
US-10-024-918-7
; Sequence 7, Application US/10024918
; Patent No. US20020168718A1
; GENERAL INFORMATION:
; APPLICANT: Hubbard, Jeffrey
; APPLICANT: Schense, Jason
; APPLICANT: Zisch, Andreas
; APPLICANT: Hall, Helke
; TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
; FILE REFERENCE: CIT 2606 CIP
; CURRENT APPLICATION NUMBER: US/10/024,918
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heparin-binding sequence from fibronectin
US-10-024-918-7

Query Match      68.0%; Score 17; DB 9; Length 6;
Best Local Similarity 75.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
Db 3 RARV 6

RESULT 4
US-09-887-469-20
; Sequence 20, Application US/09887469
; Patent No. US20020146433A1
; GENERAL INFORMATION:
; APPLICANT: Krempel, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; FILE REFERENCE: 15280-424-1US
; CURRENT APPLICATION NUMBER: US/09/887,469
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20

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; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Respiratory Syncytial Virus
US-09-887-469-20

Query Match      68.0%; Score 17; DB 10; Length 6;
Best Local Similarity 75.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RARI 5
Db 1 RARV 4

RESULT 5
US-09-802-077-59
; Sequence 59, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 59
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-59

Query Match      64.0%; Score 16; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRA 3
Db 1 PRA 3

RESULT 6
US-09-802-096-59
; Sequence 59, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amen
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07

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; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 59
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-59

Query Match
  64.0%; Score 16; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRA 3
DB 1 PRA 3

RESULT 7
US-10-036-418-17
; Sequence 17, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetulus
US-10-036-418-17

Query Match
  64.0%; Score 16; DB 12; Length 6;
Best Local Similarity 60.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRARI 5
DB 2 PSSRI 6

RESULT 8
US-10-036-418-18
; Sequence 18, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetulus
US-10-036-418-18

Query Match
  64.0%; Score 16; DB 12; Length 6;
Best Local Similarity 60.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

; PRIOR APPLICATION NUMBER: US 09/800,433
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-800-433-5

Query Match
  56.0%; Score 14; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAR 4
DB 3 RAR 5

RESULT 11
US-10-066-151-5
; Sequence 5, Application US/10066151
; Patent No. US20020132300A1
; GENERAL INFORMATION:
; APPLICANT: Hogan, Patrick G.
; APPLICANT: Rao, Anjana
; TITLE OF INVENTION: SPECIFIC INHIBITORS OF NFAT ACTIVATION
; TITLE OF INVENTION: BY CALCINEURIN AND THEIR USE IN TREATING IMMUNE-RELATED
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 10861-004002
; CURRENT APPLICATION NUMBER: US/10/066,151
; CURRENT FILING DATE: 2002-01-31
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/074,467
; PRIOR FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-151-5

Query Match
  60.0%; Score 15; DB 12; Length 6;
Best Local Similarity 60.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PRARI 5
DB 1 PRIEI 5

RESULT 10
US-09-800-433-5
; Sequence 5, Application US/09800433
; Patent No. US20020106378A1
; GENERAL INFORMATION:
; APPLICANT: O'Hare and Elliott
; TITLE OF INVENTION: Materials and methods for intracellular transport and
; FILE REFERENCE: 49408
; CURRENT APPLICATION NUMBER: US/09/800,433
; CURRENT FILING DATE: 2000-03-05
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/395,344
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-800-433-5

Query Match
  56.0%; Score 14; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAR 4
DB 3 RAR 5

RESULT 11
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US-09-800-433-7
; Sequence 7, Application US/09800433
; Patent No. US20020106378A1
; GENERAL INFORMATION:
; APPLICANT: O'Hare and Elliott
; TITLE OF INVENTION: Materials and methods for intracellular transport and
; TITLE OF INVENTION: their uses
; FILE REFERENCE: 49408
; CURRENT APPLICATION NUMBER: US/09/800,433
; PRIOR FILING DATE: 2000-03-05
; PRIOR APPLICATION NUMBER: 09/395,344
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-800-433-7
Query Match 56.0%; Score 14; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RAR 4
Db 3 RAR 5
RESULT 12
US-09-977-831-19
; Sequence 19, Application US/09977831
; Patent No. US20020120100A1
; GENERAL INFORMATION:
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne
; APPLICANT: Bony, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 Transporter peptides
; CURRENT APPLICATION NUMBER: US/09/977,831
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: U.S.N. 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
US-09-977-831-19
Query Match 56.0%; Score 14; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RAR 4
Db 3 RAR 5
RESULT 13
US-09-947-387-47
; Sequence 47, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
US-09-800-433-7
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Mole
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735, 0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-947-387-47
Query Match 56.0%; Score 14; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 8.8e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RAR 5
Db 1 RAR 4
RESULT 14
US-09-823-823-66
; Sequence 66, Application US/09823823
; Patent No. US20020171092A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Satoshi
; APPLICANT: Kasai, Hiroaki
; APPLICANT: Nakamura, Shoko
; APPLICANT: Suzuki, Makoto
; APPLICANT: Hamada, Tohru
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USIN
; FILE REFERENCE: 12817-004001
; CURRENT APPLICATION NUMBER: US/09/823,823
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/208,688
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: JP 97/343316
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 66
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated protein
US-09-823-823-66
Query Match 56.0%; Score 14; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RAR 4
Db 3 RAR 5
RESULT 15
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US-09-904-599A-3
; Sequence 3, Application US/09904599A
; Patent No. US20020076419A1
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.,
; APPLICANT: Engler, Jeffrey A.
; TITLE OF INVENTION: Ligands Added to Adenovirus Fiber
; FILE REFERENCE: D5839/D
; CURRENT APPLICATION NUMBER: US/09/904,599A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 08/218,369
; PRIOR FILING DATE: 1994-03-28
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide that can be added to the c-terminus
; OTHER INFORMATION: of the fiber protein without interfering
; OTHER INFORMATION: with trimerization
US-09-904-599A-3
Query Match 56.0%; Score 14; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 RAR 4
Db 3 RAR 5

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Search completed: December 12, 2002, 15:21:21
Job time : 5.25 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:58 ; Search time 11 Seconds
(without alignments)
43.697 Million cell updates/sec

Title: US-09-600-432-39

Perfect score: 25

Sequence: 1 PRARI 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

pir_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	52.0	5	2 S62883	seminal plasma pro
2	12	48.0	4	2 A02147	phagocytosis-stimu
3	12	48.0	5	2 B22565	R-phycocerythrin al
4	12	48.0	6	2 PT0618	T-cell receptor be
5	11	44.0	4	2 PT0721	peptidyl-di-peptida
6	11	44.0	5	2 JN0860	pyruvate kinase (E
7	10	40.0	6	2 A11490	orf 3 rara 5'-regi
8	10	40.0	6	4 SI5596	protamine P1 - ora
9	9	36.0	4	2 I37013	protamine P1 - Cer
10	9	36.0	4	2 I84439	protamine P1 - sav
11	9	36.0	5	2 C41225	copper resistance
12	9	36.0	5	2 I40702	primase - Citrobac
13	9	36.0	5	2 I39964	ribosomal protein
14	9	36.0	5	2 I39966	ribosomal protein
15	9	36.0	5	2 I39965	ribosomal protein
16	9	36.0	6	2 PC4127	hypothetical 6 pro
17	9	36.0	6	2 B60110	repetitive protein
18	9	36.0	6	2 A61140	sperm acrosomal pr
19	9	36.0	6	2 I37027	protamine P1 - gor
20	9	36.0	6	2 B33932	ig mu chain d regi
21	9	36.0	6	2 PT0518	T-cell receptor be
22	9	36.0	6	2 PT0568	T-cell receptor be
23	9	36.0	6	2 SI1556	hydrogensulfite re
24	8	32.0	6	2 A13765	hypothetical prote
25	8	32.0	6	2 A37765	transferrin - bovi
26	8	32.0	6	2 A19780	thyroliberin - bovi
27	7	28.0	3	3 RHTDNO	thyroliberin - pig
28	7	28.0	3	3 RUPGT	thyroliberin - she
29	7	28.0	3	3 RUSHT	thyroliberin - she

30	7	28.0	3	3 A92971	thyroliberin - eas
31	7	28.0	3	3 A33802	thyrotropin-releas
32	7	28.0	3	3 A43391	TRH-like tripeptid
33	7	28.0	3	3 I78890	tyrosine protein k
34	7	28.0	4	2 A32039	tyrosine-melanocyt
35	7	28.0	4	2 PL0140	carbon-monoxide de
36	7	28.0	4	2 S53508	starvation-induced
37	7	28.0	4	2 SI7255	ribosomal protein
38	7	28.0	4	2 A34626	RECH-related neuro
39	7	28.0	4	2 I51049	metallothionein-A
40	7	28.0	4	2 PT0240	ig heavy chain CRD
41	7	28.0	4	2 I34357	schwannomin - mous
42	7	28.0	4	2 PT0697	T-cell receptor be
43	7	28.0	4	2 PT0675	T-cell receptor be
44	7	28.0	5	1 HOROHA	proctolin - Americ
45	7	28.0	5	2 A60521	glycogen phosphory

ALIGNMENTS

RESULT 1

S62883

seminal plasma protein II - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S62883

R:Romero, A.; Varela, P.F.; Sanz, L.; Toepfer-Petersen, E.; Calvete, J.J.

FEBS Lett. 382, 15-17, 1996

A:Title: Crystallization and preliminary X-ray diffraction analysis of boar seminal p

A:Reference number: S62882; MUID:96196555; PMID:8612739

A:Accession: S62883

A:Molecule type: protein

A:Residues: 1-5 <ROW>

C:Complex: heterodimer; seminal plasma protein I and seminal plasma protein II

C:Keywords: glycoprotein; heterodimer; semen

Query Match 52.0%; Score 13; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ARI 5

Db 1 ARI 3

RESULT 2

A02147

phagocytosis-stimulating peptide (tuftsin) - human

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 03-Feb-1994

C:Accession: A02147

R:Nishioka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.

Biochem. Biophys. Res. Commun. 47, 172-179, 1972

A:Title: The characteristics, isolation and synthesis of the phagocytosis stimulating

A:Reference number: A02147; MUID:72187087; PMID:4112769

A:Accession: A02147

A:Molecule type: protein

A:Residues: 1-4 <NIS>

A:Note: a peptide having the same structure, physical properties, and biological acti

R:Fidalgo, B.V.; Najjar, V.A.

Biochemistry 6, 3386-3392, 1967

A:Reference number: A37502; MUID:68091045; PMID:4169272

A:Contents: annotation; immunoglobulin class

C:Comment: An Igg (called leucokinin) binds reversibly to the cell membrane of neutro

n is essential for maximum stimulation of the phagocytic activity of neutrophils.

C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 48.0%; Score 12; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PR 2

Db 3 PR 4
||
RESULT 3
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: B22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: B22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>
Query Match 48.0%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PR 2
||
Db 4 PR 5
||
RESULT 4
PT0618
T-cell receptor beta chain V-D-J region (120-2CK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0618
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0618
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor
Query Match 48.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PR 2
||
Db 4 PR 5
||
RESULT 5
PT0721
T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0721
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0721
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor
Query Match 44.0%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ARI 5
||
Db 1 ARL 3
||
RESULT 6
JN0860
peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito
C:Species: Sarda orientalis (striped bonito)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: JN0860
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide
A:Reference number: JN0859; MUID:94080036; PMID:7764272
A:Accession: JN0860
A:Molecule type: protein
A:Residues: 1-5 <MAT>
A:Experimental source: intestine
C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme inhibitor
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor
Query Match 44.0%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PRA 3
||
Db 3 PHA 5
||
RESULT 7
A11490
pyruvate kinase (EC 2.7.1.40) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Mar-1995
C:Accession: A11490
R:Hjeltnist, G.; Andersson, J.; Edlund, B.; Engstrom, L.
Biochem. Biophys. Res. Commun. 61, 559-563, 1974
A:Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate kinase
A:Reference number: A11490; MUID:75127438; PMID:4375989
A:Accession: A11490
A:Molecule type: protein
A:Residues: 1-6 <HJE>
A:Experimental source: liver
C:Keywords: glycolysis; phosphotransferase
Query Match 40.0%; Score 10; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 RARI 5
||
Db 3 RASL 6
||
RESULT 8
S15596
orf 3 rara 5'-region - human
C:Species: Homo sapiens (man)
C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C:Accession: S15596
R:Brand, N.J.; Petkovich, M.; Chambon, P.
Nucleic Acids Res. 18, 6799-6806, 1990
A:Title: Characterization of a functional promoter for the human retinoic acid receptor
A:Reference number: S15594; MUID:91088249; PMID:2175878
A:Accession: S15596
A:Molecule type: DNA
A:Residues: 1-6 <BRA>
A:Cross-references: EMBL:X56058; NID:g35876
A:Note: this ORF from Fig. 2 is not annotated in GenBank entry HSPARA2, release 111.0

C:Comment: This sequence is not thought to be translated.

C:Genetics:

A:Gene: GBH:RARA

A:Cross-references: GDB:120337; OMIM:180240

A:Map position: 17q12-17q12

Query Match 40.0%; Score 10; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 PRA 3
| |
Db 3 PSA 5

RESULT 9

161883

Protamine P1 - orangutan (fragment)

C:Species: Pongo pygmaeus (orangutan)

C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000

C:Accession: I61883

R:Queralt, R.; Oliva, R.

Gene 133, 197-204, 1993

A:Title: Identification of conserved potential regulatory sequences of the protamine-end

A:Reference number: I37013; MUID:94040810; PMID:8224908

A:Accession: I61883

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Cross-references: EMBL:Z12146; NID:g38156; PIDN:CAA78130.1; PID:g4379372

Query Match 36.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AR 4
| |
Db 2 AR 3

RESULT 10

I37013

Protamine P1 - Cercopithecus patas (fragment)

C:Species: Cercopithecus patas

C:Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000

C:Accession: I37013

R:Queralt, R.; Oliva, R.

Gene 133, 197-204, 1993

A:Title: Identification of conserved potential regulatory sequences of the protamine-end

A:Reference number: I37013; MUID:94040810; PMID:8224908

A:Accession: I37013

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Cross-references: EMBL:Z12150; NID:g22814; PIDN:CAA78134.1; PID:g4377415

Query Match 36.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AR 4
| |
Db 2 AR 3

RESULT 11

I84439

Protamine P1 - savannah baboon (fragment)

C:Species: Papio hamadryas doguera (savannah baboon)

C:Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000

C:Accession: I84439

R:Queralt, R.; Oliva, R.

Gene 133, 197-204, 1993

A:Title: Identification of conserved potential regulatory sequences of the protamine-

A:Reference number: I37013; MUID:94040810; PMID:8224908

A:Accession: I84439

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Cross-references: EMBL:Z12147; NID:g38134; PIDN:CAA78131.1; PID:g4379349

Query Match 36.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AR 4
| |
Db 2 AR 3

RESULT 12

C41225

copper resistance protein - Pseudomonas syringae pv. tomato (fragment)

C:Species: Pseudomonas syringae pv. tomato

C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993

C:Accession: C41225

R:Cha, J.S.; Cooksey, D.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991

A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer

A:Reference number: A41225; MUID:92020961; PMID:1924351

A:Accession: C41225

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 <CHA>

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PR 2
|:
Db 2 PR 3

RESULT 13

I40702

primase - Citrobacter diversus (fragment)

C:Species: Citrobacter diversus

C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Aug-1996

C:Accession: I40702

R:Versalovic, J.; Lupski, J.R.

Mol. Microbiol. 8, 343-355, 1993

A:Title: Conservation and evolution of the rpsU-dnaG-rpoD macromolecular synthesis (M

A:Reference number: I40702; MUID:93302510; PMID:8316085

A:Accession: I40702

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: GB:I01754; NID:g144439

C:Genetics:

A:Gene: dnaG

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RI 5
| |
Db 4 RI 5

RESULT 14

I39964

ribosomal protein S4 - Bacillus circulans (fragment)

C:Species: Bacillus circulans

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996

C:Accession: I39964
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
C:Accession: I39964
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99041; NID:g143471
C:Genetics:
A:Gene: rpsD

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AR 4
||
Db 2 AR 3

RESULT 15
I39966
ribosomal protein S4 - Bacillus licheniformis (fragment)
C:Species: Bacillus licheniformis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39966
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735; PMID:1400226
C:Accession: I39966
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99043; NID:g143475
C:Genetics:
A:Gene: rpsD

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AR 4
||
Db 2 AR 3

Search completed: December 12, 2002, 15:20:09
Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:38 ; Search time 6 Seconds
(without alignments)
34.564 Million cell updates/sec

Title: US-09-600-432-39

Perfect score: 25

Sequence: 1 PRARI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	12	48.0	4	1 TUFT_HUMAN	P01858 homo sapien
2	9	36.0	4	1 FYRI_ANCEL	P58706 anthopleura
3	8	32.0	6	1 UN06_CLOPA	P81351 clostridium
4	7	28.0	3	1 THYL_PIG	P01151 sus scrofa
5	7	28.0	4	1 DCML_PSECH	P19316 pseudomonas
6	7	28.0	4	1 RM01_YEAST	P36515 saccharomyc
7	7	28.0	4	1 BP07_BOTIN	P30425 bothrops in
8	7	28.0	5	1 EI03_LITRU	P82099 litoria rub
9	7	28.0	5	1 PAP2_PARMA	P81864 pardachirus
10	7	28.0	5	1 PRCT_PERAM	P01373 periplaneta
11	7	28.0	5	1 SUGA_ACHDO	P19991 acheta dome
12	7	28.0	6	1 CIP1_MYTED	P13736 mytilus edu
13	7	28.0	6	1 CIP2_MYTED	P13737 mytilus edu
14	7	28.0	6	1 EI01_LITRU	P82096 litoria rub
15	7	28.0	6	1 TM0F_LEPDE	P42985 leptinotars
16	7	28.0	6	1 TM0F_SARBU	P41495 sarcophaga
17	7	28.0	6	1 TRP1_PSEPU	P36414 herpes simp
18	7	28.0	6	1 VP19_HSV1K	P23210 herpes simp
19	6	24.0	4	1 DCMS_PSECH	P19918 pseudomonas
20	6	24.0	4	1 FFAA_ANCEL	P58705 anthopleura
21	5	20.0	4	1 FAR3_HIRME	P42562 hirudo medi
22	5	20.0	4	1 FAR4_HIRME	P42563 hirudo medi
23	5	20.0	4	1 FLRF_HIRME	P42561 hirudo medi
24	5	20.0	4	1 FLRN_ANCEL	P58707 anthopleura
25	5	20.0	4	1 FMRF_MACNI	P01162 macrocallis
26	5	20.0	5	1 FARP_ARTTR	P41853 artiposthi
27	5	20.0	5	1 UF01_MOUSE	P38639 mus musculu
28	5	20.0	6	1 ACPH_RABIT	P25154 oryctolagus
29	5	20.0	6	1 FARP_MONEX	P41966 moniezia ex
30	4	16.0	3	1 LOXE_VIRFI	P24722 vibrio fisc
31	4	16.0	4	1 ACHI_ACHFU	P35904 achatina fu
32	4	16.0	5	1 BIOB_CITFR	P12997 citrobacter
33	4	16.0	5	1 EI04_LITRU	P82100 litoria rub

34	4	16.0	5	1 PSK_DAUCA	P58261 daucus caro
35	4	16.0	5	1 RE11_LITRU	P82070 litoria rub
36	4	16.0	5	1 RE21_LITRU	P82071 litoria rub
37	4	16.0	5	1 RE31_LITRU	P82072 litoria rub
38	4	16.0	5	1 UC22_MAIZE	P80628 zea mays (m
39	4	16.0	6	1 LOK1_LOCM1	P41491 locusta mig
40	3	12.0	4	1 E0S1_HUMAN	P02731 homo sapien
41	3	12.0	5	1 RE32_LITRU	P82073 litoria rub
42	3	12.0	5	1 TP1S_CANPA	P54714 canis famil
43	2	8.0	3	1 GR0W_HUMAN	P01157 homo sapien
44	2	8.0	5	1 AL14_CARMA	P81817 carcinus ma
45	2	8.0	5	1 TRM3_ECOLI	P13973 escherichia

ALIGNMENTS

RESULT 1					
ID	TUFT_HUMAN	STANDARD;	PRT;	4 AA.	
AC	P01858;				
DT	21-JUL-1986 (Rel. 01, Created)				
DE	16-OCT-2001 (Rel. 40, Last annotation update)				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
RW	NCBI_TaxID=9606;				
[1]					
SEQUENCE.					
RP	MEDLINE=72187087; PubMed=4112769;				
RA	Nishio K., Constantopoulos A., Satoh P.S., Najjar V.A.;				
RT	"The characteristics, isolation and synthesis of the phagocytosis				
RL	stimulating peptide tuftsin.";				
RL	Biochem. Biophys. Res. Commun. 47:172-179(1972).				
[2]					
RP	IMMUNOGLOBULIN CLASS.				
FX	MEDLINE=68091045; PubMed=4169272;				
RA	Fidalgo B.V., Najjar V.A.;				
RT	"The physiological role of the lymphoid system. VI. The stimulatory				
RL	effect of leucophilic gamma globulin (leucokinin) on the phagocytic				
RL	activity of human polymorphonuclear leucocyte.";				
CC	Biochemistry 6:3386-3392(1967).				
CC	-1- MISCELLANEOUS: AN ICG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE				
CC	CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE				
CC	MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.				
CC	TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC				
CC	ACTIVITY OF NEUTROPHILS.				
DR	PIR; A02147; A02147.				
DR	MIN; 191150; --				
SQ	SEQUENCE 4 AA; 501 MW; 74176321C00000000 CRC64;				

Query Match 48.0%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 PR 2
DB	3 PR 4

RESULT 2					
ID	FYRI_ANCEL	STANDARD;	PRT;	4 AA.	
AC	P58706;				
DT	15-JUN-2002 (Rel. 41, Created)				
DE	15-JUN-2002 (Rel. 41, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Ancho-Ramide I [contains: Ancho-Ramide III].				
OS	Anthopleura elegantissima (Sea anemone).				
OC	Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinoptaria;				
OC	Nynanthaeae; Actiniidae; Anthopleura.				

FT MOD_RES 3 3 AMIDATION.
SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000000 CRC64;
Query Match 28.0%; Score 7; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 P 1
Db 3 P 3
RESULT 5
DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CUII.
OS Pseudomonas carboxydhydrogena.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendick I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydrotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -|- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -|- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -|- COFACTOR: Molybdenum (molybdopterin).
CC -|- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR; F0140; P10140.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F000000000000 CRC64;
Query Match 28.0%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 P 1
Db 4 P 4
RESULT 6
RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YML1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Gromann L., Graack H.-R., Kruff V., Choll T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal

RT subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
DR PIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D000000000000 CRC64;
Query Match 28.0%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 P 1
Db 4 P 4
RESULT 7
BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Bradykinin-potentiatng peptide S5.2 (5A) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:231-227(1990).
CC -|- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B000000000000 CRC64;
Query Match 28.0%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 P 1
Db 5 P 5
RESULT 8
EI03_LITRU STANDARD; PRT; 5 AA.
AC P82099;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;

CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL
CC PIR; JS0319;
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDBH00000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1
|
Db 4 P 4

RESULT 12
CIP1_MYTED
ID CIP1_MYTED STANDARD; PRT; 6 AA.
AC P13736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide I (MIP I).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE-Pedal ganglion;
RX MEDLINE=88240357; PubMed=337776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN MUSCLES.
CC -!- SIMILARITY: TO MIP II.
KW PIR; A27696; A27696.
DR Hormone; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1
|
Db 3 P 3

RESULT 13
CIP2_MYTED
ID CIP2_MYTED STANDARD; PRT; 6 AA.
AC P13737;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide II (MIP II).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE-Pedal ganglion;
RX MEDLINE=88240357; PubMed=337776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN MUSCLES.
CC -!- SIMILARITY: TO MIP I.
KW PIR; B27696; B27696.

KW Hormone; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1
|
Db 3 P 3

RESULT 14
EI01_LITRU
ID EI01_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electrin I.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodytidae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE-Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog Litoria electrica. Comparison with the skin peptides from Litoria rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: SECRETED.
KW Amphibian skin; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1
|
Db 3 P 3

RESULT 15
OVM_LEPDE
ID OVM_LEPDE STANDARD; PRT; 6 AA.
AC P42985;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Oviductal motility stimulating peptide (LeD-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phycophaga; Chrysomeloidea; Chrysomelidae;
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RX MEDLINE=91271080; PubMed=2052497;
RA Spittsels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
RA Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility stimulating head peptide in the Colorado potato beetle, Leptinotarsa decemlineata.";
RL Peptides 12:31-36(1991).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE

CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;
AMIDATION.
Query Match 28.0%; Score 7; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 P 1
Db 5 P 5

Search completed: December 12, 2002, 15:19:18
Job time : 6 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:09:54 ; Search time 21.25 Seconds
(without alignments)
48.482 Million cell updates/sec

Title: US-09-600-432-39
Perfect score: 25
Sequence: 1 PRARI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPTEMBL21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	7	28.0	5	13 P83308	P83308 gallus gall
2	7	28.0	6	10 P82181	P82181 spinacia ol
3	7	28.0	6	10 P82182	P82182 spinacia ol
4	6	24.0	6	10 P82541	P82541 spinacia ol
5	4	16.0	5	10 Q99007	Q99007 bordeum vul
6	3	12.0	4	11 Q08433	Q08433 rattus norv
7	2	8.0	5	2 P83073	P83073 bacillus ce

ALIGNMENTS

RESULT 1
P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;

DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE FMRamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE, AND SYNTHESIS.
RP TISSUE-BRAIN;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by antibodies to FMRamide.";
RL Nature 305:328-330(1983).
CC 1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC 1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE) FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;
Query Match 28.0%; Score 7; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 P 1
DB 2 P 2
RESULT 2
P82181 ID P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
DT 01-JUN-2000 (Tremblrel. 14, Created)
DT 01-JUN-2000 (Tremblrel. 14, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC 1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC 1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC 1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC 1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC 1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR001790; Ribosomal_L10
DR Pfam: PF00466; Ribosomal_L10eub.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
Query Match 28.0%; Score 7; DB 10; Length 6;
Best Local Similarity 33.3%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 2 RAR 4
DB 4 RTK 6

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CC CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC InterPro: IPR002222; Ribosomal_S19.
DR Pfam: PF00203; Ribosomal_S19; PARTIAL.
DR PRINTS: PR00975; RIBOSOMALS19; PARTIAL.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 24.0%; Score 6; DB 10; Length 6;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RA 3
DB 2 RS 3

RESULT 5
Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1) (Fragment).
GN AMY1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RP SEQUENCE FROM N.A.
RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V.; Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers."
RL Plant Mol. Biol. 16:713-721(1991).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
CC EMBL; X54643; CAA38455.1;
DR Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON_TER 5
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 16.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 A 3
DB 2 A 2

RESULT 6
Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)
DE (Fragment).
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10116;
 [1]

RN SEQUENCE FROM N.A.
 RP STRAIN=GUNN;
 RC MEDLINE=91282758; PubMed=1840486;
 RX Sato H., Aono S., Kashiwamata S., Koiwai O.;
 RA "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 RT hyperbilirubinemic Gunn rat.";
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS.
 CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR
 CC -!- BETA-D-GLUCURONOSIDE.
 CC -!- SUBCELLULAR LOCATION: MICROSOME.
 DR EMBL; S38636; AAB19259.1; -;
 KW Transferase; Glycosyltransferase; Microsome; Multigene family.
 FT NON_TER 1 1
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 12.0%; Score 3; DB 11; Length 4;
 Best Local Similarity 0.0%; Pred. No. 6.7e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 I 5
 ;
 Db 2 V 2

RESULT 7

P83073
 ID P83073 PRELIMINARY; PRT; 5 AA.
 AC P83073;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE 88 kDa protein (Fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 8.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 6.7e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
 ;
 Db 2 K 2

Search completed: December 12, 2002, 15:18:47
 Job time : 22.25 secs

